

(AP), which can be used to produce a nucleoside 5'-phosphate ester from the corresponding nucleoside when a phosphate donor, e.g. poly-, phenyl-, or carbamyl-phosphoric acid, is reacted in its presence at pH 3.0 to 5.5. The PA can be used for the economic and efficient production of nucleoside 5'-phosphate esters for use as condiments, pharmaceuticals and intermediates for pharmaceuticals

Sequence 249 AA;

Query Match 100.0%; Score 1190; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 5.2e-119;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LALVATGNDTTPKPDLYLKNSEAINSLALPPPAVGSIAPLNDQMYEGRLRNTTER 60
DB 19 LALVATGNDTTPKPDLYLKNSEAINSLALPPPAVGSIAPLNDQMYEGRLRNTTER 78
QY 61 GKLAEDANLSSGGVANAFAFGSPITTEKDAPALHKLNTMIEDAGDLATRSKDHMR 120
DB 79 GKLAEDANLSSGGVANAFAFGSPITTEKDAPALHKLNTMIEDAGDLATRSKDHMR 138
QY 121 IRPFAFYGVSTCTTTEODKLSKNGSYPSGHTSIGMATLVLAETINPQRONEILKRGYELG 180
DB 139 IRPFAFYGVSTCTTTEODKLSKNGSYPSGHTSIGMATLVLAETINPQRONEILKRGYELG 198
QY 181 QSRVICGYHMQSDVDARVVGSAVVATLHTNPAFQOOLQAKAEFAHQHKK 231
DB 199 QSRVICGYHMQSDVDARVVGSAVVATLHTNPAFQOOLQAKAEFAHQHKK 249

RESULT 2

AAW71029
ID AAW71029 standard; protein; 249 AA.

AC AAW71029;

DT 21-OCT-1998 (first entry)

DE Acid phosphatase enzyme amino acid sequence.

KW Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning; intermediate.

OS Escherichia blattae.

PH Key Location/Qualifiers

FT Peptide 1..18

FT Protein /note= "signal peptide" 19..249

FT /note= "mature protein; Claim 6"

EP857788-A2.

PD 12-AUG-1998.

PF 20-NOV-1997; 97EP-00309365.

PR 21-NOV-1996; 96JP-00311103.

PR 18-JUN-1997; 97JP-00161674.

PA (AJIN) AJINOMOTO CO INC.

PI Mihara Y, Utagawa T, Yamada H, Asano Y;

DR WPI; 1998-416010/36.

DR N-PSDB; AAV43046.

PT Preparation of nucleoside 5'-phosphates comprises reacting nucleoside with phosphate donor in presence of acid phosphatase - used as seasonings or pharmaceutical intermediates.

PS Example 12; Page 35-36; 83pp; English.

CC The present sequence represents an acid phosphatase enzyme. The CC specification describes a method for the preparation of nucleoside 5'-phosphate esters. The method comprises reacting a nucleoside with a CC phosphate donor at pH 3.0-5.5 in the presence of an acid phosphatase that CC has been altered to increase its affinity for the nucleoside and/or to CC increase its thermal stability, or in the presence of a microorganism CC that has been transformed with recombinant DNA containing a gene coding CC for such an acid phosphatase. Nucleoside 5'-phosphates are useful as CC seasonings or pharmaceuticals or as intermediates for them

Sequence 249 AA;

Query Match 100.0%; Score 1190; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 5.2e-119;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LALVATGNDTTPKPDLYLKNSEAINSLALPPPAVGSIAPLNDQMYEGRLRNTTER 60
DB 19 LALVATGNDTTPKPDLYLKNSEAINSLALPPPAVGSIAPLNDQMYEGRLRNTTER 78
QY 61 GKLAEDANLSSGGVANAFAFGSPITTEKDAPALHKLNTMIEDAGDLATRSKDHMR 120
DB 79 GKLAEDANLSSGGVANAFAFGSPITTEKDAPALHKLNTMIEDAGDLATRSKDHMR 138
QY 121 IRPFAFYGVSTCTTTEODKLSKNGSYPSGHTSIGMATLVLAETINPQRONEILKRGYELG 180
DB 139 IRPFAFYGVSTCTTTEODKLSKNGSYPSGHTSIGMATLVLAETINPQRONEILKRGYELG 198
QY 181 QSRVICGYHMQSDVDARVVGSAVVATLHTNPAFQOOLQAKAEFAHQHKK 231
DB 199 QSRVICGYHMQSDVDARVVGSAVVATLHTNPAFQOOLQAKAEFAHQHKK 249

RESULT 3

AAB75064
ID AAB75064 standard; protein; 249 AA.

AC AAB75064;

DT 23-JUN-2001 (first entry)

DE Escherichia blattae nucleoside-5'-phosphate producing enzyme protein.

KW Variant nucleoside-5'-phosphate producing enzyme; mutagenesis; transphosphorylation; phosphatase; protein co-ordinate data;

KW X-ray structural analysis; three-dimensional structure.

OS Escherichia blattae.

PN WO200118184-A1.

PD 15-MAR-2001.

PF 01-SEP-2000; 2000MO-JP005973.

PR 03-SEP-1999; 99JP-00249545.

PA (AJIN) AJINOMOTO CO INC.

PI Ishikawa K, Suzuki E, Gondoh K, Shimda N, Mihara Y, Kawasaki H;

PI Kurahashi O, Konda T, Shimaoka M, Kozutsumi R, Asano Y;

DR WPI; 2001-380914/40.

DR N-PSDB; AAH19701.

PT Variant enzyme having elevated nucleoside 5'-prime phosphate producing activity and having a specific three-dimensional structure for production of nucleotides as pharmaceutical intermediates.

PS Disclosure; Page 107; 150pp; Japanese.

CC The present invention describes a variant nucleoside-5'-phosphate producing enzyme which is a modification of a transphosphorylase or

CC phosphatase which contains a lysine, two arginine and two histidine
CC residues and in which the C-alpha distances between these residues are
CC enclosing a space which permits the binding of a nucleoside with these
CC residues. Also described are: (1) a gene encoding the variant enzyme; (2)
CC expression vectors containing the DNA; (3) host cells transformed by the
CC vectors; (4) preparation of the variant enzyme by culture of the
CC transformants; (5) crystals of the enzyme and of a complex of the enzyme
CC with molybdenic acid; and (6) selection of inhibitors of acid phosphatase
CC or transphosphorylase using the structural coordinates derived from the
CC enzyme. The variant enzymes with increased efficiency for production of
CC nucleoside 5'-phosphates can be used as pharmaceutical intermediates.
CC AAH19701 to AAH19785 and AAB75064 to AAB75101 represent sequences used in
CC the exemplification of the present invention

SQ Sequence 249 AA;

Query Match 100.0%; Score 1190; DB 4; Length 249;
Best Local Similarity 100.0%; Pred. No. 5.2e-119;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LALVATGNDTTTKPDLVYLYKNSSEAINSLALPPPAVGSIAFLNDQAMYEQRLRNTER 60
DB 19 LALVATGNDTTTKPDLVYLYKNSSEAINSLALPPPAVGSIAFLNDQAMYEQRLRNTER 78
QY 61 GKLAEDANLSSGGVANAFAFGSPITEKDA PALHKLITNMIEDAGLATRSADHYMR 120
DB 79 GKLAEDANLSSGGVANAFAFGSPITEKDA PALHKLITNMIEDAGLATRSADHYMR 138
QY 121 IRPFAFYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLAELNPOQNEILKRGYELG 180
DB 139 IRPFAFYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLAELNPOQNEILKRGYELG 198
QY 181 OSRVICGYHMOSDVAARVGSAAVATLTHTNPAFQOOLQKAKAEPAQHOKK 231
DB 199 OSRVICGYHMOSDVAARVGSAAVATLTHTNPAFQOOLQKAKAEPAQHOKK 249

RESULT 4

AAW71034
ID AAW71034 standard; protein; 231 AA.

AC AAW71034;
XX
DT 21-OCT-1998 (first entry)
XX
DE Mutant acid phosphatase enzyme of Escherichia blattae.
XX
KW Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
KW mutant; intermediate.
XX
OS Synthetic.
OS Escherichia blattae.
XX
FH Key Location/Qualifiers
FT Misc-difference 74
FT /label= G74D
XX
XX EP857788-A2.
XX
XX 12-AUG-1998.
XX
XX 20-NOV-1997; 97EP-00309365.
XX
XX 21-NOV-1996; 96JP-00311103.
XX PR 18-JUN-1997; 97JP-00161674.
XX
XX (AJIN) AJINOMOTO CO INC.
XX
XX Mihiara Y, Utagawa T, Yamada H, Asano Y;
XX WPI, 1998-416010/36.
XX
XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside

PT with phosphate donor in presence of acid phosphatase - used as seasonings
PT or pharmaceutical intermediates.

PS Example 19; Page; 83pp; English.

XX AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
XX created using the mature protein of AAW71029. The specification describes
XX a method for the preparation of nucleoside 5'-phosphate esters. The
XX method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
XX 5.5 in the presence of an acid phosphatase that has been altered to
XX increase its affinity for the nucleoside and/or to increase its thermal
XX stability, or in the presence of a microorganism that has been
XX transformed with recombinant DNA containing a gene coding for such an
XX acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
XX pharmaceuticals or as intermediates for them. note: this sequence does
XX not appear in the specification; it was created using information
XX provided

SQ Sequence 231 AA;

Query Match 99.4%; Score 1183; DB 2; Length 231;
Best Local Similarity 99.6%; Pred. No. 2.6e-118;
Matches 230; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LALVATGNDTTTKPDLVYLYKNSSEAINSLALPPPAVGSIAFLNDQAMYEQRLRNTER 60
DB 1 LALVATGNDTTTKPDLVYLYKNSSEAINSLALPPPAVGSIAFLNDQAMYEQRLRNTER 60
QY 61 GKLAEDANLSSGGVANAFAFGSPITEKDA PALHKLITNMIEDAGLATRSADHYMR 120
DB 61 GKLAEDANLSSGGVANAFAFGSPITEKDA PALHKLITNMIEDAGLATRSADHYMR 120
QY 121 IRPFAFYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLAELNPOQNEILKRGYELG 180
DB 121 IRPFAFYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLAELNPOQNEILKRGYELG 180
QY 181 OSRVICGYHMOSDVAARVGSAAVATLTHTNPAFQOOLQKAKAEPAQHOKK 231
DB 181 OSRVICGYHMOSDVAARVGSAAVATLTHTNPAFQOOLQKAKAEPAQHOKK 231

RESULT 5

AAW71035
ID AAW71035 standard; protein; 231 AA.

AC AAW71035;
XX
DT 21-OCT-1998 (first entry)
XX
DE Mutant acid phosphatase enzyme of Escherichia blattae.
XX
KW Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
KW mutant; intermediate.
XX
OS Synthetic.
OS Escherichia blattae.
XX
FH Key Location/Qualifiers
FT Misc-difference 74
FT /label= G74D
FT Misc-difference 153
FT /label= 1153T
XX
XX EP857788-A2.
XX
XX 12-AUG-1998.
XX
XX 20-NOV-1997; 97EP-00309365.
XX
XX 21-NOV-1996; 96JP-00311103.
XX PR 18-JUN-1997; 97JP-00161674.
XX
XX (AJIN) AJINOMOTO CO INC.
XX

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XX MIhara Y, Utogawa T, Yamada H, Asano Y;
XX WPI; 1998-416010/36.
XX
XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
XX with phosphate donor in presence of acid phosphatase - used as seasonings
XX or pharmaceutical intermediates.
XX
XX Example 19; Page; 83pp; English.
XX
CC AAW7034-42 represent mutant acid phosphatase enzymes. The mutants were
CC created using the mature protein of AAW71029. The specification describes
CC a method for the preparation of nucleoside 5'-phosphate esters. The
CC method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
CC 5.5 in the presence of an acid phosphatase that has been altered to
CC increase its affinity for the nucleoside and/or to increase its thermal
CC stability, or in the presence of a microorganism that has been
CC transformed with recombinant DNA containing a gene coding for such an
CC acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
CC pharmaceuticals or as intermediates for them. note: this sequence does
CC not appear in the specification; it was created using information
CC provided
XX
XX Sequence 231 AA;
SQ
Query Match          99.0%; Score 1178; DB 2; Length 231;
Best Local Similarity 99.1%; Pred. No. 9.1e-118;
Matches 229; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 LALVATGNDTTTTPDLYYLKNSSEAINSLALPPPPVAGSIAFLNDQAMTEQGRLLNTER 60
DB 1 LALVATGNDTTTTPDLYYLKNSSEAINSLALPPPPVAGSIAFLNDQAMTEQGRLLNTER 60
QY 61 GKLAEDANLSSGCVANAFSGAFSGPITEKADAPALHKLITNMIEDAGDLATRSADHYMR 120
DB 61 GKLAEDANLSSGCVANAFSGAFSGPITEKADAPALHKLITNMIEDAGDLATRSADHYMR 120
QY 121 IRPFAFYGVSTGNTTODKLSKNGSYPSGHTSIGMTALVLAINEPQRONEILKRGYELG 180
DB 121 IRPFAFYGVSTGNTTODKLSKNGSYPSGHTSIGMTALVLAINEPQRONEILKRGYELG 180
QY 181 QSRVICGYHMOSDVAARVGSAAVATLTNPAPFOOQOKKAEFAOHOXK 231
DB 181 QSRVICGYHMOSDVAARVGSAAVATLTNPAPFOOQOKKAEFAOHOXK 231

RESULT 6
AAW71036
ID AAW71036 standard; protein; 231 AA.
XX
XX AAW71036;
XX
XX 21-OCT-1998 (first entry)
XX
XX Mutant acid phosphatase enzyme of Escherichia blattae.
XX
XX Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
XX mutant; intermediate.
XX
XX Synthetic.
XX
XX Escherichia blattae.
XX
XX Key Location/Qualifiers
XX
XX Misc-difference 63 /label= L63Q
XX
XX Misc-difference 65 /label= A65Q
XX
XX Misc-difference 66 /label= E66A
XX
XX Misc-difference 74 /label= G74D
XX
XX Misc-difference 153

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FT /label= I153T
XX
XX EP857788-A2.
XX
XX 12-AUG-1998.
XX
XX 20-NOV-1997; 97BP-00309365.
XX
XX 21-NOV-1996; 96JP-00311103.
XX
XX 18-JUN-1997; 97JP-00161674.
XX
XX (AJIN ) AJINOMOTO CO INC.
XX
XX MIhara Y, Utogawa T, Yamada H, Asano Y;
XX WPI; 1998-416010/36.
XX
XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
XX with phosphate donor in presence of acid phosphatase - used as seasonings
XX or pharmaceutical intermediates.
XX
XX Example 19; Page; 83pp; English.
XX
CC AAW7034-42 represent mutant acid phosphatase enzymes. The mutants were
CC created using the mature protein of AAW71029. The specification describes
CC a method for the preparation of nucleoside 5'-phosphate esters. The
CC method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
CC 5.5 in the presence of an acid phosphatase that has been altered to
CC increase its affinity for the nucleoside and/or to increase its thermal
CC stability, or in the presence of a microorganism that has been
CC transformed with recombinant DNA containing a gene coding for such an
CC acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
CC pharmaceuticals or as intermediates for them. note: this sequence does
CC not appear in the specification; it was created using information
CC provided
XX
XX Sequence 231 AA;
SQ
Query Match          97.6%; Score 1161; DB 2; Length 231;
Best Local Similarity 97.8%; Pred. No. 6.1e-116;
Matches 226; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 LALVATGNDTTTTPDLYYLKNSSEAINSLALPPPPVAGSIAFLNDQAMTEQGRLLNTER 60
DB 1 LALVATGNDTTTTPDLYYLKNSSEAINSLALPPPPVAGSIAFLNDQAMTEQGRLLNTER 60
QY 61 GKLAEDANLSSGCVANAFSGAFSGPITEKADAPALHKLITNMIEDAGDLATRSADHYMR 120
DB 61 GKLAEDANLSSGCVANAFSGAFSGPITEKADAPALHKLITNMIEDAGDLATRSADHYMR 120
QY 121 IRPFAFYGVSTGNTTODKLSKNGSYPSGHTSIGMTALVLAINEPQRONEILKRGYELG 180
DB 121 IRPFAFYGVSTGNTTODKLSKNGSYPSGHTSIGMTALVLAINEPQRONEILKRGYELG 180
QY 181 QSRVICGYHMOSDVAARVGSAAVATLTNPAPFOOQOKKAEFAOHOXK 231
DB 181 QSRVICGYHMOSDVAARVGSAAVATLTNPAPFOOQOKKAEFAOHOXK 231

RESULT 7
AAW71037
ID AAW71037 standard; protein; 231 AA.
XX
XX AAW71037;
XX
XX 21-OCT-1998 (first entry)
XX
XX Mutant acid phosphatase enzyme of Escherichia blattae.
XX
XX Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
XX mutant; intermediate.
XX
XX Synthetic.

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OS Escherichia blattae.

XX Key Location/Qualifiers

FT Misc-difference 63

FT Misc-difference /label= L63Q

FT Misc-difference 65

FT Misc-difference /label= A65Q

FT Misc-difference 66

FT Misc-difference /label= B66A

FT Misc-difference 74

FT Misc-difference /label= G74D

FT Misc-difference 85

FT Misc-difference /label= S85Y

FT Misc-difference 153

FT Misc-difference /label= I153T

XX EP857788-A2.

XX 12-AUG-1998.

XX 20-NOV-1997; 97BP-00309365.

XX 21-NOV-1996; 96JP-00311103.

XX 18-JUN-1997; 97JP-00161674.

XX (AJIN) AJINOMOTO CO INC.

XX Minhara Y, Utagawa T, Yamada H, Asano Y;

XX WPI, 1998-416010/36.

XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside

XX with phosphate donor in presence of acid phosphatase - used as seasonings

XX or pharmaceutical intermediates.

XX Example 19; Page; 83pp; English.

XX AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were

XX created using the mature protein of AAW71029. The specification describes

XX a method for the preparation of nucleoside 5'-phosphate esters. The

XX method comprises reacting a nucleoside with a phosphate donor at pH 3.0-

XX 5.5 in the presence of an acid phosphatase that has been altered to

XX increase its affinity for the nucleoside and/or to increase its thermal

XX stability, or in the presence of a microorganism that has been

XX transformed with recombinant DNA containing a gene coding for such an

XX acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or

XX pharmaceuticals or as intermediates for them. note: this sequence does

XX not appear in the specification; it was created using information

XX provided

XX Sequence 231 AA;

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RESULT 8

AAW71038

XX ID AAW71038 standard; protein; 231 AA.

XX AC AAW71038;

XX 21-OCT-1998 (first entry)

XX Mutant acid phosphatase enzyme of Escherichia blattae.

XX Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;

XX mutant; intermediate.

XX Synthetic.

XX Escherichia blattae.

XX OS

XX Key Location/Qualifiers

FT Misc-difference 63

FT Misc-difference /label= L63Q

FT Misc-difference 65

FT Misc-difference /label= A65Q

FT Misc-difference 66

FT Misc-difference /label= B66A

FT Misc-difference 74

FT Misc-difference /label= G74D

FT Misc-difference 135

FT Misc-difference /label= T135K

FT Misc-difference 136

FT Misc-difference /label= E136D

FT Misc-difference 153

FT Misc-difference /label= I153T

XX EP857788-A2.

XX 12-AUG-1998.

XX 20-NOV-1997; 97BP-00309365.

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XX 18-JUN-1997; 97JP-00161674.

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XX a method for the preparation of nucleoside 5'-phosphate esters. The

XX method comprises reacting a nucleoside with a phosphate donor at pH 3.0-

XX 5.5 in the presence of an acid phosphatase that has been altered to

XX increase its affinity for the nucleoside and/or to increase its thermal

XX stability, or in the presence of a microorganism that has been

XX transformed with recombinant DNA containing a gene coding for such an

XX acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or

XX pharmaceuticals or as intermediates for them. note: this sequence does

XX not appear in the specification; it was created using information

XX provided

XX Sequence 231 AA;

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AAW71038

XX ID AAW71038 standard; protein; 231 AA.

XX AC AAW71038;

XX 21-OCT-1998 (first entry)

XX Mutant acid phosphatase enzyme of Escherichia blattae.

XX Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;

XX mutant; intermediate.

XX Synthetic.

XX Escherichia blattae.

XX OS

XX Key Location/Qualifiers

FT Misc-difference 63

FT Misc-difference /label= L63Q

FT Misc-difference 65

FT Misc-difference /label= A65Q

FT Misc-difference 66

FT Misc-difference /label= B66A

FT Misc-difference 74

FT Misc-difference /label= G74D

FT Misc-difference 135

FT Misc-difference /label= T135K

FT Misc-difference 136

FT Misc-difference /label= E136D

FT Misc-difference 153

FT Misc-difference /label= I153T

XX EP857788-A2.

XX 12-AUG-1998.

XX 20-NOV-1997; 97BP-00309365.

XX 21-NOV-1996; 96JP-00311103.

XX 18-JUN-1997; 97JP-00161674.

XX (AJIN) AJINOMOTO CO INC.

XX Minhara Y, Utagawa T, Yamada H, Asano Y;

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XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside

XX with phosphate donor in presence of acid phosphatase - used as seasonings

XX or pharmaceutical intermediates.

XX Example 19; Page; 83pp; English.

XX AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were

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XX increase its affinity for the nucleoside and/or to increase its thermal

XX stability, or in the presence of a microorganism that has been

XX transformed with recombinant DNA containing a gene coding for such an

XX acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or

XX pharmaceuticals or as intermediates for them. note: this sequence does

XX not appear in the specification; it was created using information

XX provided

XX Sequence 231 AA;

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AAW71038

XX ID AAW71038 standard; protein; 231 AA.

XX AC AAW71038;

XX 21-OCT-1998 (first entry)

XX Mutant acid phosphatase enzyme of Escherichia blattae.

XX Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;

XX mutant; intermediate.

XX Synthetic.

XX Escherichia blattae.

XX OS

XX Key Location/Qualifiers

FT Misc-difference 63

FT Misc-difference /label= L63Q

FT Misc-difference 65

FT Misc-difference /label= A65Q

FT Misc-difference 66

FT Misc-difference /label= B66A

FT Misc-difference 74

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Db      1 LALVATGNDTTTKDLYLKNSEAINSLALPPPAVGSIAFLNDQAMTEQGRLLNTER 60
Qy      61 GKLAEDANLSSGGVANAFAFGAFSPITTEKDAAPALHKLNTNMIEDAGDLATRSKDHMYR 120
Db      61 GKQAQADANLSSGGVANAFAFGAFSPITTEKDAAPALHKLNTNMIEDAGDLATRSKDHMYR 120
Qy      121 IRPPAFYGVSTCNTTEEDDKLSKNGSYPSGHTSIGMATLVLAETNPORONEILKRGYEIG 180
Db      121 IRPPAFYGVSTCNTTKDDKLSKNGSYPSGHTSIGMATLVLAETNPORONEILKRGYEIG 180
Qy      181 QSRVTCGYHMQSDVDARVVGSAVVATLTHTNPAFQOOLQAKAEFAQHOKK 231
Db      181 QSRVTCGYHMQSDVDARVVGSAVVATLTHTNPAFQOOLQAKAEFAQHOKK 231

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RESULT 9 AAW71039

ID AAW71039 standard; protein; 231 AA.

AC AAW71039;

DT 21-OCT-1998 (first entry)

DE Mutant acid phosphatase enzyme of Escherichia blattae.

KW Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning; mutant; intermediate.

OS Synthetic.

OS Escherichia blattae.

FT Key Location/Qualifiers

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FT      63 /label= L63Q
FT      65 /label= A65Q
FT      66 /label= E66A
FT      69 /label= N69D
FT      71 /label= S71A
FT      72 /label= S72A
FT      74 /label= G74D
FT      135 /label= T135K
FT      136 /label= E136D
FT      153 /label= I153T

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EP857788-A2.

12-AUG-1998.

20-NOV-1997; 97EP-00309365.

21-NOV-1996; 96JP-00311103.

18-JUN-1997; 97JP-00161674.

(AJIN) AJINOMOTO CO INC.

MIhara Y, Utogawa T, Yamada H, Asano Y;

WPI; 1998-416010/36.

Preparation of nucleoside 5'-phosphates comprises reacting nucleoside with phosphate donor in presence of acid phosphatase - used as seasonings or pharmaceutical intermediates.

PS Example 19; Page; 83pp; English.

CC AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were created using the mature protein of AAW71029. The specification describes a method for the preparation of nucleoside 5'-phosphate esters. The method comprises reacting a nucleoside with a phosphate donor at pH 3.0-5.5 in the presence of an acid phosphatase that has been altered to increase its affinity for the nucleoside and/or to increase its thermal stability, or in the presence of a microorganism that has been transformed with recombinant DNA containing a gene coding for such an acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or pharmaceuticals or as intermediates for them. note: this sequence does not appear in the specification; it was created using information provided

CC Sequence 231 AA;

Query Match 95.9%; Score 1141; DB 2; Length 231;

Best Local Similarity 95.7%; Pred. No. 8.6e-114;

Matches 221; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

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Qy      1 LALVATGNDTTTKDLYLKNSEAINSLALPPPAVGSIAFLNDQAMTEQGRLLNTER 60
Db      1 LALVATGNDTTTKDLYLKNSEAINSLALPPPAVGSIAFLNDQAMTEQGRLLNTER 60
Qy      61 GKLAEDANLSSGGVANAFAFGAFSPITTEKDAAPALHKLNTNMIEDAGDLATRSKDHMYR 120
Db      61 GKQAQADANLSSGGVANAFAFGAFSPITTEKDAAPALHKLNTNMIEDAGDLATRSKDHMYR 120
Qy      121 IRPPAFYGVSTCNTTEEDDKLSKNGSYPSGHTSIGMATLVLAETNPORONEILKRGYEIG 180
Db      121 IRPPAFYGVSTCNTTKDDKLSKNGSYPSGHTSIGMATLVLAETNPORONEILKRGYEIG 180
Qy      181 QSRVTCGYHMQSDVDARVVGSAVVATLTHTNPAFQOOLQAKAEFAQHOKK 231
Db      181 QSRVTCGYHMQSDVDARVVGSAVVATLTHTNPAFQOOLQAKAEFAQHOKK 231

```

RESULT 10

ID AAW71040 standard; protein; 231 AA.

AC AAW71040;

DT 21-OCT-1998 (first entry)

DE Mutant acid phosphatase enzyme of Escherichia blattae.

KW Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning; mutant; intermediate.

OS Synthetic.

OS Escherichia blattae.

FT Key Location/Qualifiers

```

FT      63 /label= L63Q
FT      65 /label= A65Q
FT      66 /label= E66A
FT      69 /label= N69D
FT      71 /label= S71A
FT      72 /label= S72A
FT      74 /label= G74D
FT      116 /label= D116B
FT      135 /label= T135K

```

```
FT Misc-difference 136
FT /label= E136D
FT Misc-difference 153
FT /label= I153T
XX
XX EP857788-A2.
XX
XX 12-AUG-1998.
XX
XX 20-NOV-1997; 97EP-00309365.
XX
XX 21-NOV-1996; 96JP-00311103.
XX 18-JUN-1997; 97JP-00161674.
XX
XX (AJIN ) AJINOMOTO CO INC.
XX
XX Mihara Y, Utagawa T, Yamada H, Asano Y;
XX
XX WPI; 1998-416010/36.
XX
XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
XX with phosphate donor in presence of acid phosphatase - used as seasonings
XX or pharmaceutical intermediates.
XX
XX Example 19; Page: 83pp; English.
XX
XX AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
XX created using the mature protein of AAW71029. The specification describes
XX a method for the preparation of nucleoside 5'-phosphate esters. The
XX method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
XX 5.5 in the presence of an acid phosphatase that has been altered to
XX increase its affinity for the nucleoside and/or to increase its thermal
XX stability, or in the presence of a microorganism that has been
XX transformed with recombinant DNA containing a gene coding for such an
XX acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
XX pharmaceuticals or as intermediates for them. note: this sequence does
XX not appear in the specification; it was created using information
XX provided
XX
XX Sequence 231 AA;
SQ
Query Match 95.5%; Score 1137; DB 2; Length 231;
Best Local Similarity 95.2%; Pred. No. 2.3e-113;
Matches 220; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 1 LALVATGNDTTTKDLYLYLKNSSEAINSLALPPPPAVGSIAFNDQAMYEGRLLRNTER 60
DB 1 LALVATGNDTTTKDLYLYLKNSSEAINSLALPPPPAVGSIAFNDQAMYEGRLLRNTER 60
QY 61 GKLAEDANLSSGCVANAFSGAFSGPITEKDAHALHKLTTWTEPAGDLATRSADHYMR 120
DB 61 GKQAQADADLAAGDVANAFSGAFSGPITEKDAHALHKLTTWTEPAGDLATRSADHYMR 120
QY 121 IRPFAFYGVSTCNTTEODPKLSKNGSPSGHTSIGWATLVLAIEINPORONEILKRGYELG 180
DB 121 IRPFAFYGVSTCNTTEODPKLSKNGSPSGHTSIGWATLVLAIEINPORONEILKRGYELG 180
QY 181 QSRVYICGVHWSQDVDAARVGSAAVVALHTNPAFOQOLQKAAEFAQHOKK 231
DB 181 QSRVYICGVHWSQDVDAARVGSAAVVALHTNPAFOQOLQKAAEFAQHOKK 231
RESULT 11
AAW71041
ID AAW71041 standard; protein; 231 AA.
XX
XX AAW71041;
XX
XX 21-OCT-1998 (first entry)
XX
XX Mutant acid phosphatase enzyme of Escherichia blattae.
XX
XX Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
```

```
KW mutant; intermediate.
XX
XX Synthetic.
OS Escherichia blattae.
XX
XX Key Location/Qualifiers
XX FH Misc-difference 63
XX FT /label= L63Q
XX FT Misc-difference 65
XX FT /label= A65Q
XX FT Misc-difference 66
XX FT /label= B66A
XX FT Misc-difference 69
XX FT /label= N69D
XX FT Misc-difference 71
XX FT /label= S71A
XX FT Misc-difference 72
XX FT /label= S72A
XX FT Misc-difference 74
XX FT /label= G74D
XX FT Misc-difference 116
XX FT /label= D116E
XX FT Misc-difference 130
XX FT /label= S130E
XX FT Misc-difference 135
XX FT /label= T135K
XX FT Misc-difference 136
XX FT /label= E136D
XX FT Misc-difference 153
XX FT /label= I153T
XX
XX EP857788-A2.
XX
XX 12-AUG-1998.
XX
XX 20-NOV-1997; 97EP-00309365.
XX
XX 21-NOV-1996; 96JP-00311103.
XX 18-JUN-1997; 97JP-00161674.
XX
XX (AJIN ) AJINOMOTO CO INC.
XX
XX Mihara Y, Utagawa T, Yamada H, Asano Y;
XX
XX WPI; 1998-416010/36.
XX
XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
XX with phosphate donor in presence of acid phosphatase - used as seasonings
XX or pharmaceutical intermediates.
XX
XX Example 19; Page: 83pp; English.
XX
XX AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
XX created using the mature protein of AAW71029. The specification describes
XX a method for the preparation of nucleoside 5'-phosphate esters. The
XX method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
XX 5.5 in the presence of an acid phosphatase that has been altered to
XX increase its affinity for the nucleoside and/or to increase its thermal
XX stability, or in the presence of a microorganism that has been
XX transformed with recombinant DNA containing a gene coding for such an
XX acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
XX pharmaceuticals or as intermediates for them. note: this sequence does
XX not appear in the specification; it was created using information
XX provided
XX
XX Sequence 231 AA;
SQ
Query Match 95.2%; Score 1133; DB 2; Length 231;
Best Local Similarity 94.8%; Pred. No. 6.3e-113;
Matches 219; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
QY 1 LALVATGNDTTTKDLYLYLKNSSEAINSLALPPPPAVGSIAFNDQAMYEGRLLRNTER 60
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```

Db      1  LALVATGNDTTTKPDLYLYLNKSEAINSLALPPPPAVGSIATFNDQMYEQRLNTER 60
Qy      61  GKLAEDANLSSGGVANAFAFGSPITTEKDA PALHKLNTMIEDAGDLATRSKCHYMR 120
        61  GKQAQADADLAAGVANAFAFGSPITTEKDA PALHKLNTMIEDADLATRSKCHYMR 120
Db      121  IRPPAFYGVSTCTNTTEBODKLSKNGSPSGHTSIGMATALVLAETINPORONEILKRGYEIG 180
Qy      121  IRPPAFYGVSTCTNTTEBODKLSKNGSPSGHTSIGMATALVLAETINPORONEILKRGYEIG 180
        121  IRPPAFYGVSTCTNTTEBODKLSKNGSPSGHTSIGMATALVLAETINPORONEILKRGYEIG 180
Qy      181  QSRVTCGYHWSQDVDAARVGVSAVATLTHTNPAFQOOLQKAKKAFQHQK 231
        181  QSRVTCGYHWSQDVDAARVGVSAVATLTHTNPAFQOOLQKAKKAFQHQK 231
        181  QSRVTCGYHWSQDVDAARVGVSAVATLTHTNPAFQOOLQKAKKAFQHQK 231

RESULT 12
AAW71042
ID  AAW71042 standard; protein; 231 AA.
AC  AAW71042;
XX
XX  21-OCT-1998 (first entry)
XX
DE  Mutant acid phosphatase enzyme of Escherichia blattae.
KM  Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
    mutant; intermediate.
XX
XX  Synthetic.
XX  Escherichia blattae.
OS
OS
XX
XX  Key
FH  Location/Qualifiers
FT  Misc-difference 63
    /label= L63Q
FT  Misc-difference 65
    /label= A65Q
FT  Misc-difference 66
    /label= E66A
FT  Misc-difference 69
    /label= N69D
FT  Misc-difference 71
    /label= S71A
FT  Misc-difference 72
    /label= S72A
FT  Misc-difference 74
    /label= G74D
FT  Misc-difference 92
    /label= A92S
FT  Misc-difference 94
    /label= A94B
FT  Misc-difference 116
    /label= D116E
FT  Misc-difference 135
    /label= T135K
FT  Misc-difference 136
    /label= E136D
FT  Misc-difference 153
    /label= I153T
XX
XX  EP857788-A2.
XX
XX  12-AUG-1998.
XX
XX  20-NOV-1997; 97EP-00309365.
XX
XX  21-NOV-1996; 96JP-00311103.
XX  18-JUN-1997; 97JP-00161674.
XX
XX  (AJIN) AJINOMOTO CO INC.
XX  Mihara Y, Utagawa T, Yamada H, Asano Y;
XX  WPI; 1998-416010/36.

```

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XX
XX  Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
PT  with phosphate donor in presence of acid phosphatase - used as seasonings
XX  or pharmaceutical intermediates.
XX
XX  Example 19; Page; 83pp; English.
PS
XX  AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
CC  created using the mature protein of AAW71029. The specification describes
CC  a method for the preparation of nucleoside 5'-phosphate esters. The
CC  method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
CC  5.5 in the presence of an acid phosphatase and/or to increase its thermal
CC  stability, or in the presence of a microorganism that has been
CC  transformed with recombinant DNA containing a gene coding for such an
CC  acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
CC  pharmaceuticals or as intermediates for them. note: this sequence does
CC  not appear in the specification; it was created using information
CC  provided
XX
XX  Sequence 231 AA;
SQ

```

```

Query Match      94.9%; Score 1129; DB 2; Length 231;
Best Local Similarity 94.4%; Pred. No. 1.7e-112;
Matches 218; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

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Qy      1  LALVATGNDTTTKPDLYLYLNKSEAINSLALPPPPAVGSIATFNDQMYEQRLNTER 60
Db      1  LALVATGNDTTTKPDLYLYLNKSEAINSLALPPPPAVGSIATFNDQMYEQRLNTER 60
Qy      61  GKLAEDANLSSGGVANAFAFGSPITTEKDA PALHKLNTMIEDAGDLATRSKCHYMR 120
        61  GKQAQADADLAAGVANAFAFGSPITTEKDA PALHKLNTMIEDAGDLATRSKCHYMR 120
Db      121  IRPPAFYGVSTCTNTTEBODKLSKNGSPSGHTSIGMATALVLAETINPORONEILKRGYEIG 180
Qy      121  IRPPAFYGVSTCTNTTEBODKLSKNGSPSGHTSIGMATALVLAETINPORONEILKRGYEIG 180
        121  IRPPAFYGVSTCTNTTEBODKLSKNGSPSGHTSIGMATALVLAETINPORONEILKRGYEIG 180
Db      181  QSRVTCGYHWSQDVDAARVGVSAVATLTHTNPAFQOOLQKAKKAFQHQK 231
Qy      181  QSRVTCGYHWSQDVDAARVGVSAVATLTHTNPAFQOOLQKAKKAFQHQK 231
        181  QSRVTCGYHWSQDVDAARVGVSAVATLTHTNPAFQOOLQKAKKAFQHQK 231

```

```

RESULT 13
AB061416
ID  AB061416 standard; protein; 253 AA.
XX
XX  AB061416;
AC
XX  29-JUL-2004 (first entry)
XX
XX  Klebsiella pneumoniae polypeptide seqid 7933.
DE
XX  Klebsiella pneumoniae polypeptide seqid 7933.
XX
XX  Recombinant expression vector; transcription regulatory element;
KM  Klebsiella pneumoniae protein; antibacterial; Vaccine.
XX
XX  Klebsiella pneumoniae.
OS
XX  US6610836-B1.
XX
XX  26-AUG-2003.
XX
XX  27-JAN-2000; 2000US-00489039.
XX
XX  29-JAN-1999; 99US-0117747P.
XX
XX  (GENO-) GENOME THERAPEUTICS CORP.
XX
XX  Breton GL, Osborne M;
XX  WPI; 2003-895346/82.
XX  N-PSDB; ACH94967.
XX

```


PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
PT preparing a vaccine composition against Klebsiella pneumoniae.
XX
XX
PS Disclosure; SEQ ID NO 7933; 932pp; English.
XX
XX The invention describes a new isolated nucleic acid encoding a Klebsiella
CC pneumoniae polypeptide. Also described are: a recombinant expression
CC vector comprising the nucleic acid, operably linked to a transcription
CC regulatory element; and a cell comprising the recombinant expression
CC vector. The nucleic acid is useful for preparing a vaccine composition
CC against Klebsiella pneumoniae. This is the amino acid sequence of a
CC Klebsiella pneumoniae polypeptide of the invention
XX
SQ Sequence 253 AA;

Query Match 92.1%; Score 1096; DB 7; Length 253;
Best Local Similarity 92.1%; Pred. No. 6.9e-109;
Matches 211; Conservative 9; Mismatches 9; Indels 0; Gaps 0;
QY 2 ALVATGNDTTTKPDLYLKNSEAINSLALPPPAVGSIAPLNDQAMYEQGRLLNTERG 61
DB 25 ALVPGNDVTTKPDLYLKNQALDLSLALPPPAVGSIAPLNDQAMYEQGRLLNTERG 84
QY 62 KLAEDANLSSGVANAFSGAFSPITEKDA PALHKLITNMIEDAGDLATRSADHYMRI 121
DB 85 KLAEDANLSSGVANAFSGAFSPITEKDA PALHKLITNMIEDAGDLATRSADHYMRI 144
QY 122 RPPAFYGVSTCNTTTEODKLKNGSYPSGHTSIGMTALVLAELNFORONEILKRGYEIQ 181
DB 145 RPPAFYGVSTCNTTTEODKLKNGSYPSGHTSIGMTALVLAELNFORONEILKRGYEIQ 204
QY 182 SRVIGCYMOSDVPDAARVGSAAVATLHTNPAFOOQLOKAKAEFAHOX 230
DB 205 SRVIGCYMOSDVPDAARVGSAAVATLHTNPAFOOQLOKAKAEFAHOX 253

RESULT 14
AAW06458
ID AAW06458 standard; protein; 248 AA.
XX
XX AAW06458;
AC
XX 13-AUG-1997 (first entry)
DT
XX
DE Enterobacter aerogenes IFO 12010 acid phosphatase.
XX
XX IFO 12010; acid phosphatase; production; nucleoside; 5'-phosphate; ester;
KW condiment; pharmaceutical; intermediate.
XX
XX Enterobacter aerogenes.
OS
XX
FH Key Location/Qualifiers
FT Misc-difference 92 /note="optionally replaced by another amino acid"
FT Misc-difference 171 /note="optionally replaced by another amino acid"
FT
XX W09637603-A1.
XX
XX 28-NOV-1996.
PD
XX
XX 24-MAY-1996; 96MO-JP001402.
PF
XX
XX 25-MAY-1995; 95JP-00149781.
PR
XX 26-MAR-1996; 96JP-00094680.
PR
XX (AJIN) AJINOMOTO CO INC.
PA
XX
XX Minara Y, Utagawa T, Yamada H, Asano Y;
PI
XX WPI; 1997-021215/02.
DR
XX N-PSDB; AAT45007.
XX

PT Efficient production of nucleoside 5'-phosphate - by reaction of a
PT nucleoside with a phosphoric acid donor in the presence of an acid
PT phosphate.
XX
XX Claim 3; Page 67-68; 95pp; Japanese.
XX
XX The present sequence is the Enterobacter aerogenes IFO 12010 acid
CC phosphatase (AP), which can be used to produce a nucleoside 5'-phosphate
CC ester from the corresponding nucleoside when a phosphate donor, e.g. poly
CC -, phenyl- or carbaryl-phosphoric acid, is reacted in its presence at pH
CC 3.0 to 5.5. The PA can be used for the economic and efficient production
CC of nucleoside 5'-phosphate esters for use as condiments, pharmaceuticals
CC and intermediates for pharmaceuticals
XX
SQ Sequence 248 AA;

Query Match 92.0%; Score 1095; DB 2; Length 248;
Best Local Similarity 92.1%; Pred. No. 8.5e-109;
Matches 211; Conservative 9; Mismatches 9; Indels 0; Gaps 0;
QY 2 ALVATGNDTTTKPDLYLKNSEAINSLALPPPAVGSIAPLNDQAMYEQGRLLNTERG 61
DB 20 ALVPGNDVTTKPDLYLKNQALDLSLALPPPAVGSIAPLNDQAMYEQGRLLNTERG 79
QY 62 KLAEDANLSSGVANAFSGAFSPITEKDA PALHKLITNMIEDAGDLATRSADHYMRI 121
DB 80 KLAEDANLSSGVANAFSGAFSPITEKDA PALHKLITNMIEDAGDLATRSADHYMRI 139
QY 122 RPPAFYGVSTCNTTTEODKLKNGSYPSGHTSIGMTALVLAELNFORONEILKRGYEIQ 181
DB 140 RPPAFYGVSTCNTTTEODKLKNGSYPSGHTSIGMTALVLAELNFORONEILKRGYEIQ 199
QY 182 SRVIGCYMOSDVPDAARVGSAAVATLHTNPAFOOQLOKAKAEFAHOX 230
DB 200 SRVIGCYMOSDVPDAARVGSAAVATLHTNPAFOOQLOKAKAEFAHOX 248

RESULT 15
AAW71031
ID AAW71031 standard; protein; 248 AA.
XX
XX AAW71031;
AC
XX 21-OCT-1998 (first entry)
DT
XX
DE Acid phosphatase enzyme amino acid sequence.
XX
XX Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
KW intermediate.
XX
XX Enterobacter aerogenes.
OS
XX
XX EP857788-A2.
XX
XX 12-AUG-1998.
PD
XX
XX 20-NOV-1997; 97EP-00309365.
PF
XX
XX 21-NOV-1996; 96JP-00311103.
PR
XX 18-JUN-1997; 97JP-00161674.
PR
XX (AJIN) AJINOMOTO CO INC.
PA
XX
XX Minara Y, Utagawa T, Yamada H, Asano Y;
PI
XX WPI; 1998-416010/36.
DR
XX N-PSDB; AAV43060.
DR
XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
PT with phosphate donor in presence of acid phosphatase - used as seasonings
PT or pharmaceutical intermediates.
PS Example 23; Page 44; 83pp; English.

XX The present sequence represents an acid phosphatase enzyme. The
 CC specification describes a method for the preparation of nucleoside 5'-
 CC phosphate esters. The method comprises reacting a nucleoside with a
 CC phosphate donor at pH 3.0-5.5 in the presence of an acid phosphatase that
 CC has been altered to increase its affinity for the nucleoside and/or to
 CC increase its thermal stability, or in the presence of a microorganism
 CC that has been transformed with recombinant DNA containing a gene coding
 CC for such an acid phosphatase. Nucleoside 5'-phosphates are useful as
 CC seasonings or pharmaceuticals or as intermediates for them
 XX

SQ Sequence 248 AA;

Query Match 92.0%; Score 1095; DB 2; Length 248;
 Best Local Similarity 92.1%; Pred. No. 8.5e-109;
 Matches 211; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY	2	ALVATGNDTTTTPEDLYLLKNSAINGSLALLPPPPAVGSIAPLNDQAMVEQGRLLNTERG	61
DB	20	ALVPAGNDATTKPDLYLLKNAQAIDSLALLPPPEVGVSIAPLNDQAMVEKGRLLNTERG	79
QY	62	KLAAEDANLSSGCVANAFSGAFSGPTTEKDAFALHKLNTMIEDAGDLATRSADHYMRI	121
DB	80	KLAAEDANLSSGCVANAFSSAFSGPTTEKDAFQHLKLTMTIEDAGDLATRSADHYMRI	139
QY	122	RPFAFYGVSTCTTEODKLSKNGSYPSGHTSIGMATLVLAELINPORONEILKRGYELGQ	181
DB	140	RPFAFYGVSTCTTEODKLSKNGSYPSGHTSIGMATLVLAELINPORONEILKRGYELGE	199
QY	182	SRVIGCYHWQSDVDARVGVSAVATLTHTNPAFQOOLQKAKAFPAQHOK	230
DB	200	SRVIGCYHWQSDVDARIVGSAVATLTHTNPAFQOOLQKAKDEFPAKTOK	248

Search completed: March 2, 2005, 20:22:54
 Job time : 120.268 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 2, 2005, 20:16:41 ; Search time 30.1961 Seconds
(without alignments)
571.065 Million cell updates/sec

Title: US-09-807-990A-124

Perfect score: 1190

Sequence: 1 LALVATGNDTTRKPDLYLK.....PAFOQOLQKAKAFQHQKK 231

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1190	100.0	231	US-08-750-145A-11	Sequence 11, Appl
2	1190	100.0	231	US-08-975-698A-8	Sequence 8, Appl
3	1190	100.0	231	US-09-417-090-8	Sequence 8, Appl
4	1190	100.0	231	US-09-727-578-8	Sequence 8, Appl
5	1190	100.0	249	US-08-750-145A-10	Sequence 10, Appl
6	1190	100.0	249	US-08-975-698A-7	Sequence 7, Appl
7	1190	100.0	249	US-09-417-090-7	Sequence 7, Appl
8	1190	100.0	249	US-09-727-578-7	Sequence 7, Appl
9	1096	92.1	253	US-09-489-039A-7933	Sequence 7933, Ap
10	1096	92.0	248	US-08-750-145A-20	Sequence 20, Appl
11	1095	92.0	248	US-08-975-698A-24	Sequence 24, Appl
12	1095	92.0	248	US-09-417-090-24	Sequence 24, Appl
13	1095	92.0	248	US-09-727-578-24	Sequence 24, Appl
14	1080	90.8	248	US-08-750-145A-22	Sequence 22, Appl
15	1080	90.8	248	US-08-975-698A-26	Sequence 26, Appl
16	1080	90.8	248	US-09-417-090-26	Sequence 26, Appl
17	1080	90.8	248	US-09-727-578-26	Sequence 26, Appl
18	986	82.9	248	US-08-750-145A-18	Sequence 18, Appl
19	986	82.9	248	US-08-975-698A-22	Sequence 22, Appl
20	986	82.9	248	US-09-417-090-22	Sequence 22, Appl
21	986	82.9	248	US-09-727-578-22	Sequence 22, Appl
22	969	81.4	249	US-08-750-145A-3	Sequence 3, Appl
23	969	81.4	249	US-08-975-698A-3	Sequence 3, Appl
24	969	81.4	249	US-09-417-090-3	Sequence 3, Appl
25	969	81.4	249	US-09-727-578-3	Sequence 3, Appl
26	962	80.8	229	US-08-750-145A-4	Sequence 4, Appl
27	962	80.8	229	US-08-975-698A-4	Sequence 4, Appl

28	962	80.8	229	US-09-417-090-4	Sequence 4, Appl
29	962	80.8	229	US-09-727-578-4	Sequence 4, Appl
30	768	64.5	244	US-08-750-145A-24	Sequence 24, Appl
31	768	64.5	244	US-08-975-698A-28	Sequence 28, Appl
32	768	64.5	244	US-09-417-090-28	Sequence 28, Appl
33	768	64.5	244	US-09-727-578-28	Sequence 28, Appl
34	312	26.2	252	US-07-717-332D-2	Sequence 2, Appl
35	191	16.1	428	US-09-489-039A-10941	Sequence 10941, A
36	181	15.2	253	US-09-540-236-3458	Sequence 3458, Ap
37	173.5	14.6	253	US-09-252-991A-28557	Sequence 28557, A
38	147	12.4	987	US-09-543-681A-7785	Sequence 7785, Ap
39	92.5	7.8	159	US-09-602-787A-102	Sequence 102, App
40	90.5	7.6	244	US-09-252-991A-21937	Sequence 21937, A
41	89.5	7.5	244	US-09-543-681A-4595	Sequence 4595, Ap
42	88.5	7.4	824	US-09-711-164-377	Sequence 377, App
43	88.5	7.4	1627	US-09-902-540-11280	Sequence 11280, A
44	85.5	7.2	187	US-09-328-352-7918	Sequence 7918, Ap
45	85.5	7.2	816	US-09-540-236-3443	Sequence 3443, Ap

ALIGNMENTS

RESULT 1
US-08-750-145A-11
Sequence 11, Application US/08750145A
Patent No. 6010851
GENERAL INFORMATION:
APPLICANT: MIHARA, Yasuhiro
APPLICANT: UTAGAWA, Takashi
APPLICANT: YAMADA, Hideaki
APPLICANT: ASANO, Yasuhisa
TITLE OF INVENTION: Method for Producing Nucleoside-5'-
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESS: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT, P.C.
STREET: 1755 S. JEFF. DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,145A
FILING DATE: 01-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-149781
FILING DATE: 05-May-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-094680
FILING DATE: 26-Mar-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0830-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Escherichia blactae
STRAIN: JCM 1650

US-08-750-145A-11

Query Match 100.0%; Score 1190; DB 3; Length 231;
Best Local Similarity 100.0%; Pred. No. 2.9e-130;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAIVATGNDTTTTPDLYLKNSEAINSLALPPPPVAGSIAFLNDQAMYEGRLLRNTER 60
DB 1 LAIVATGNDTTTTPDLYLKNSEAINSLALPPPPVAGSIAFLNDQAMYEGRLLRNTER 60
QY 61 GKLAADANLSSGGVANAFAFGSPITEKAPALHKLITNMIEDAGDLATRSKADHYMR 120
DB 61 GKLAADANLSSGGVANAFAFGSPITEKAPALHKLITNMIEDAGDLATRSKADHYMR 120
QY 121 IRPFAVGVSTCNTTEODKLSKNGSPSGHTSIGMATLVLAETNPORONEILRGYELG 180
DB 121 IRPFAVGVSTCNTTEODKLSKNGSPSGHTSIGMATLVLAETNPORONEILRGYELG 180
QY 181 QSRVTCGYHMOQSDVDAARVGSAAVATLTNPAPFOOLQKAKAEFAQHOKK 231
DB 181 QSRVTCGYHMOQSDVDAARVGSAAVATLTNPAPFOOLQKAKAEFAQHOKK 231

RESULT 2

US-08-975-698A-8
Sequence 8, Application US/08975698A
Patent No. 6015697

GENERAL INFORMATION:

APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA

COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,698A
FILING DATE: 21-NOV-1997
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Escherichia blattae
STRAIN: JCM 1650

US-08-975-698A-8

Query Match 100.0%; Score 1190; DB 3; Length 231;
Best Local Similarity 100.0%; Pred. No. 2.9e-130;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAIVATGNDTTTTPDLYLKNSEAINSLALPPPPVAGSIAFLNDQAMYEGRLLRNTER 60
DB 1 LAIVATGNDTTTTPDLYLKNSEAINSLALPPPPVAGSIAFLNDQAMYEGRLLRNTER 60
QY 61 GKLAADANLSSGGVANAFAFGSPITEKAPALHKLITNMIEDAGDLATRSKADHYMR 120
DB 61 GKLAADANLSSGGVANAFAFGSPITEKAPALHKLITNMIEDAGDLATRSKADHYMR 120
QY 121 IRPFAVGVSTCNTTEODKLSKNGSPSGHTSIGMATLVLAETNPORONEILRGYELG 180
DB 121 IRPFAVGVSTCNTTEODKLSKNGSPSGHTSIGMATLVLAETNPORONEILRGYELG 180
QY 181 QSRVTCGYHMOQSDVDAARVGSAAVATLTNPAPFOOLQKAKAEFAQHOKK 231
DB 181 QSRVTCGYHMOQSDVDAARVGSAAVATLTNPAPFOOLQKAKAEFAQHOKK 231

RESULT 3

US-09-417-090-8
Sequence 8, Application US/09417090
Patent No. 6207435

GENERAL INFORMATION:

APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/417,090
FILING DATE: 13-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE: 21-NOV-1997
ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Escherichia blattae
STRAIN: JCM 1650

US-09-417-090-8

Query Match 100.0%; Score 1190; DB 3; Length 231;
Best Local Similarity 100.0%; Pred. No. 2.9e-130;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAIVATGNDTTTTPDLYLKNSEAINSLALPPPPVAGSIAFLNDQAMYEGRLLRNTER 60
DB 1 LAIVATGNDTTTTPDLYLKNSEAINSLALPPPPVAGSIAFLNDQAMYEGRLLRNTER 60
QY 61 GKLAADANLSSGGVANAFAFGSPITEKAPALHKLITNMIEDAGDLATRSKADHYMR 120
DB 61 GKLAADANLSSGGVANAFAFGSPITEKAPALHKLITNMIEDAGDLATRSKADHYMR 120
QY 121 IRPFAVGVSTCNTTEODKLSKNGSPSGHTSIGMATLVLAETNPORONEILRGYELG 180
DB 121 IRPFAVGVSTCNTTEODKLSKNGSPSGHTSIGMATLVLAETNPORONEILRGYELG 180
QY 181 QSRVTCGYHMOQSDVDAARVGSAAVATLTNPAPFOOLQKAKAEFAQHOKK 231
DB 181 QSRVTCGYHMOQSDVDAARVGSAAVATLTNPAPFOOLQKAKAEFAQHOKK 231

Db 1 LALVATGNDTTTKDLYYLKNSSEAINSLALLPPPAVGSIAFLNDQAMYEGRLLRNTER 60
Qy 61 GKLAEDANLSSGGVANAFAFGSPITEKDA PALHKLTTNMIEDAGLATRSAXDHYMR 120
Db 61 GKLAEDANLSSGGVANAFAFGSPITEKDA PALHKLTTNMIEDAGLATRSAXDHYMR 120
Qy 121 IRPPAFYGVSTCNTTEODKLSKNSGSPSGHTSIGMATAVLAEINPQRONEILRGVELG 180
Db 121 IRPPAFYGVSTCNTTEODKLSKNSGSPSGHTSIGMATAVLAEINPQRONEILRGVELG 180
Qy 181 OSRVICGYHMOSDVDAARVGSAAVATLHTNPAFQOOLQKAKAEFAQHOKK 231
Db 181 OSRVICGYHMOSDVDAARVGSAAVATLHTNPAFQOOLQKAKAEFAQHOKK 231

RESULT 4
US-09-727-578-8
Sequence 8, Application US/09727578
Patent No. 6355472

GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/727,578
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Escherichia blattae
STRAIN: JCM 1650
US-09-727-578-8

Query Match 100.0%; Score 1190; DB 3; Length 231;
Best Local Similarity 100.0%; Pred. No. 2.9e-130;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LALVATGNDTTTKDLYYLKNSSEAINSLALLPPPAVGSIAFLNDQAMYEGRLLRNTER 60
Db 1 LALVATGNDTTTKDLYYLKNSSEAINSLALLPPPAVGSIAFLNDQAMYEGRLLRNTER 60
Qy 61 GKLAEDANLSSGGVANAFAFGSPITEKDA PALHKLTTNMIEDAGLATRSAXDHYMR 120

Db 61 GKLAEDANLSSGGVANAFAFGSPITEKDA PALHKLTTNMIEDAGLATRSAXDHYMR 120
Qy 121 IRPPAFYGVSTCNTTEODKLSKNSGSPSGHTSIGMATAVLAEINPQRONEILRGVELG 180
Db 121 IRPPAFYGVSTCNTTEODKLSKNSGSPSGHTSIGMATAVLAEINPQRONEILRGVELG 180
Qy 181 OSRVICGYHMOSDVDAARVGSAAVATLHTNPAFQOOLQKAKAEFAQHOKK 231
Db 181 OSRVICGYHMOSDVDAARVGSAAVATLHTNPAFQOOLQKAKAEFAQHOKK 231

RESULT 5
US-08-750-145A-10
Sequence 10, Application US/08750145A
Patent No. 6010851

GENERAL INFORMATION:
APPLICANT: MIHARA, Yasuhiro
APPLICANT: UTAGAWA, Takashi
APPLICANT: YAMADA, Hideaki
APPLICANT: ASANO, Yasuhisa
TITLE OF INVENTION: Method for Producing Nucleoside-5'-
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFF. DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,145A
FILING DATE: 01-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-149781
FILING DATE: 05-May-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-094680
FILING DATE: 26-Mar-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0830-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Escherichia blattae
STRAIN: JCM 1650
US-08-750-145A-10

Query Match 100.0%; Score 1190; DB 3; Length 249;
Best Local Similarity 100.0%; Pred. No. 3.3e-130;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LALVATGNDTTTKDLYYLKNSSEAINSLALLPPPAVGSIAFLNDQAMYEGRLLRNTER 60
Db 19 LALVATGNDTTTKDLYYLKNSSEAINSLALLPPPAVGSIAFLNDQAMYEGRLLRNTER 78
Qy 61 GKLAEDANLSSGGVANAFAFGSPITEKDA PALHKLTTNMIEDAGLATRSAXDHYMR 120

Db 79 GKLAEDANLSSGGVANAFAFGSPITEKDPALHKLITNMIEDAGDLATRSKDHMYR 138
QY 121 IRPFAFYGVSTCNTTEBDKLSKNGSYSPGHTSIGMATALVLAETINPORONEILKRGYEIG 180
Db 139 IRPFAFYGVSTCNTTEBDKLSKNGSYSPGHTSIGMATALVLAETINPORONEILKRGYEIG 198
QY 181 QSRVTCGYHMQSDVDARVGSAAVAVATLTHTNPAFQOOLQAKAEFAHQK 231
Db 199 QSRVTCGYHMQSDVDARVGSAAVAVATLTHTNPAFQOOLQAKAEFAHQK 249

RESULT 6

US-08-975-698A-7
Sequence 7, Application US/08975698A
Patent No. 6015697
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,698A
FILING DATE: 21-NOV-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Escherichia blattae
STRAIN: JCM 1650
US-08-975-698A-7

Query Match 100.0%; Score 1190; DB 3; Length 249;
Best Local Similarity 100.0%; Pred. No. 3.3e-130;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LALVATGNDTTTDPDLYLKNSSEAINSLALPPPAVGSIAFLNDQAMYEQGRLLRNTER 60
Db 19 LALVATGNDTTTDPDLYLKNSSEAINSLALPPPAVGSIAFLNDQAMYEQGRLLRNTER 78
QY 61 GKLAEDANLSSGGVANAFAFGSPITEKDPALHKLITNMIEDAGDLATRSKDHMYR 120
Db 79 GKLAEDANLSSGGVANAFAFGSPITEKDPALHKLITNMIEDAGDLATRSKDHMYR 138
QY 121 IRPFAFYGVSTCNTTEBDKLSKNGSYSPGHTSIGMATALVLAETINPORONEILKRGYEIG 180
Db 139 IRPFAFYGVSTCNTTEBDKLSKNGSYSPGHTSIGMATALVLAETINPORONEILKRGYEIG 198

QY 181 QSRVTCGYHMQSDVDARVGSAAVAVATLTHTNPAFQOOLQAKAEFAHQK 231
Db 199 QSRVTCGYHMQSDVDARVGSAAVAVATLTHTNPAFQOOLQAKAEFAHQK 249

RESULT 7

US-09-417-090-7
Sequence 7, Application US/09417090
Patent No. 6207435
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/417,090
FILING DATE: 13-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE: 21-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Escherichia blattae
STRAIN: JCM 1650
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-417-090-7

Query Match 100.0%; Score 1190; DB 3; Length 249;
Best Local Similarity 100.0%; Pred. No. 3.3e-130;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LALVATGNDTTTDPDLYLKNSSEAINSLALPPPAVGSIAFLNDQAMYEQGRLLRNTER 60
Db 19 LALVATGNDTTTDPDLYLKNSSEAINSLALPPPAVGSIAFLNDQAMYEQGRLLRNTER 78
QY 61 GKLAEDANLSSGGVANAFAFGSPITEKDPALHKLITNMIEDAGDLATRSKDHMYR 120
Db 79 GKLAEDANLSSGGVANAFAFGSPITEKDPALHKLITNMIEDAGDLATRSKDHMYR 138
QY 121 IRPFAFYGVSTCNTTEBDKLSKNGSYSPGHTSIGMATALVLAETINPORONEILKRGYEIG 180
Db 139 IRPFAFYGVSTCNTTEBDKLSKNGSYSPGHTSIGMATALVLAETINPORONEILKRGYEIG 198
QY 181 QSRVTCGYHMQSDVDARVGSAAVAVATLTHTNPAFQOOLQAKAEFAHQK 231

Db 199 OSRVICGYHWSQDVDAARVGSAAVATLHTNPAFOOOLOKAKAEPAHQKK 249

RESULT 8
US-09-727-578-7

; Sequence 7, Application US/09727578
; Patent No. 6355472
; GENERAL INFORMATION:
; APPLICANT: MIHARA, YASUHIRO
; APPLICANT: UTAGAWA, TAKASHI
; APPLICANT: YAMADA, HIDEAKI
; APPLICANT: ASANO, YASUHIKA
; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
; TITLE OF INVENTION: ESTER
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/727,578
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/975,698
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0010-0885-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 249 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Escherichia biattaee
; STRAIN: JCM 1650
; US-09-727-578-7

Query Match 100.0%; Score 1190; DB 3; Length 249;
Best Local Similarity 100.0%; Pred. No. 3,3e-130;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LALVATGNDTTTKPDLVYLKNSAENSLALPPPPAVGSIAFLNDQAMTEGRLRNTER 60
Db 19 LALVATGNDTTTKPDLVYLKNSAENSLALPPPPAVGSIAFLNDQAMTEGRLRNTER 78
Qy 61 GKLAEDANLSSGGVANAFAFGSPITEKDA PALHKLTTNMIEDAGDLATRSADHYMR 120
Db 79 GKLAEDANLSSGGVANAFAFGSPITEKDA PALHKLTTNMIEDAGDLATRSADHYMR 138
Qy 121 IRPFAFVSTCNTTEODKLSKNGSPSGHTSIGMATAVLVAEINPQRNEILKRGYELG 180
Db 139 IRPFAFVSTCNTTEODKLSKNGSPSGHTSIGMATAVLVAEINPQRNEILKRGYELG 198
Qy 181 OSRVICGYHWSQDVDAARVGSAAVATLHTNPAFOOOLOKAKAEPAHQKK 231
Db 199 OSRVICGYHWSQDVDAARVGSAAVATLHTNPAFOOOLOKAKAEPAHQKK 249

RESULT 9
US-09-489-039A-7933

; Sequence 7933, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709,2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7933
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-7933

Query Match 92.1%; Score 1096; DB 4; Length 253;
Best Local Similarity 92.1%; Pred. No. 3.1e-119;
Matches 211; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Qy 2 ALVATGNDTTTKPDLVYLKNSAENSLALPPPPAVGSIAFLNDQAMTEGRLRNTER 61
Db 25 ALVPPGNDVTTKPDLYLTNQAIDSLALPPPPAVGSIAFLNDQAMTEGRLRNTER 84
Qy 62 KLAEDANLSSGGVANAFAFGSPITEKDA PALHKLTTNMIEDAGDLATRSADHYMR 121
Db 85 KLAEDANLSSGGVANAFAFGSPITEKDA PALHKLTTNMIEDAGDLATRSADHYMR 144
Qy 122 RPPAFVSTCNTTEODKLSKNGSPSGHTSIGMATAVLVAEINPQRNEILKRGYELG 181
Db 145 RPPAFVSTCNTTEODKLSKNGSPSGHTSIGMATAVLVAEINPQRNEILKRGYELG 204
Qy 182 SRVICGYHWSQDVDAARVGSAAVATLHTNPAFOOOLOKAKAEPAHQKK 230
Db 205 SRVICGYHWSQDVDAARVGSAAVATLHTNPAFOOOLOKAKAEPAHQKK 253

RESULT 10
US-08-750-145A-20

; Sequence 20, Application US/08750145A
; Patent No. 6010851
; GENERAL INFORMATION:
; APPLICANT: MIHARA, Yasuhiro
; APPLICANT: UTAGAWA, Takashi
; APPLICANT: YAMADA, Hideaki
; APPLICANT: ASANO, Yasuhisa
; TITLE OF INVENTION: Method for Producing Nucleoside-5'-
; TITLE OF INVENTION: Phosphate Ester
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 S. JEFF. DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,145A
; FILING DATE: 01-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-149781
; FILING DATE: 05-May-1995

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 8-094680
 FILING DATE: 26-Mar-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: NORMAN F. OBLON
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 0010-0830-0 PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-413-3000
 TELEFAX: 703-413-2220
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 248 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 ORGANISM: Enterobacter aerogenes
 STRAIN: IFO 12010
 US-08-750-145A-20

Query Match 92.0%; Score 1095; DB 3; Length 248;
 Best Local Similarity 92.1%; Pred. No. 3.9e-119;
 Matches 211; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 2 ALVATGNDTTTKPDLYYLNKSEAINSLALPPPPAVGSIAFLNDQAMYEQRLNTERG 61
 DB 20 ALVPGNDATTKPDLYYLNKQAIDSLALPPPEVGSIAFLNDQAMYEKGLNTERG 79
 QY 62 KLAEDANLSSGVANAFSGAFSGSPITEKDAPLHKLITNMIEDAGLATRSADHYMRI 121
 DB 80 KLAEDANLSSGVANAFSGAFSGSPITEKDAPLHKLITNMIEDAGLATRSADHYMRI 139
 QY 122 RPPAFYGVSTCNTTEQDKLSKNGSYPSGHTSIGMATLVLAETNPORONEILKRGYELGQ 181
 DB 140 RPPAFYGVSTCNTTEQDKLSKNGSYPSGHTSIGMATLVLAETNPORONEILKRGYELG 199
 QY 182 SRVIGYHWSQDVDAARVGSAAVATLTNPAPFOOLQKAKDEFQK 230
 DB 200 SRVIGYHWSQDVDAARVGSAAVATLTNPAPFOOLQKAKDEFQK 248

RESULT 11
 US-08-975-698A-24
 Sequence 24, Application US/08975698A
 Patent No. 6015657
 GENERAL INFORMATION:
 APPLICANT: MIHARA, YASUHIRO
 APPLICANT: UTAGAWA, TAKASHI
 APPLICANT: YAMADA, HIDEAKI
 APPLICANT: ASANO, YASUHIISA
 TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
 STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: USA
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/975,698A
 FILING DATE: 21-NOV-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: OBLON, NORMAN F
 REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 0010-0885-0
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 413-3000
 TELEFAX: (703) 413-2220
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 248 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 ORGANISM: Enterobacter aerogenes
 STRAIN: IFO 12010
 US-08-975-698A-24

Query Match 92.0%; Score 1095; DB 3; Length 248;
 Best Local Similarity 92.1%; Pred. No. 3.9e-119;
 Matches 211; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 2 ALVATGNDTTTKPDLYYLNKSEAINSLALPPPPAVGSIAFLNDQAMYEQRLNTERG 61
 DB 20 ALVPGNDATTKPDLYYLNKQAIDSLALPPPEVGSIAFLNDQAMYEKGLNTERG 79
 QY 62 KLAEDANLSSGVANAFSGAFSGSPITEKDAPLHKLITNMIEDAGLATRSADHYMRI 121
 DB 80 KLAEDANLSSGVANAFSGAFSGSPITEKDAPLHKLITNMIEDAGLATRSADHYMRI 139
 QY 122 RPPAFYGVSTCNTTEQDKLSKNGSYPSGHTSIGMATLVLAETNPORONEILKRGYELGQ 181
 DB 140 RPPAFYGVSTCNTTEQDKLSKNGSYPSGHTSIGMATLVLAETNPORONEILKRGYELG 199
 QY 182 SRVIGYHWSQDVDAARVGSAAVATLTNPAPFOOLQKAKDEFQK 230
 DB 200 SRVIGYHWSQDVDAARVGSAAVATLTNPAPFOOLQKAKDEFQK 248

RESULT 12
 US-09-417-090-24
 Sequence 24, Application US/09417090
 Patent No. 6207435
 GENERAL INFORMATION:
 APPLICANT: MIHARA, YASUHIRO
 APPLICANT: UTAGAWA, TAKASHI
 APPLICANT: YAMADA, HIDEAKI
 APPLICANT: ASANO, YASUHIISA
 TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
 STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: USA
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/417,090
 FILING DATE: 13-OCT-1999
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/975,698
 FILING DATE: 21-NOV-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: OBLON, NORMAN F
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 0010-0885-0
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Enterobacter aerogenes
STRAIN: IFO 12010
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-417-090-24

Query Match 92.0%; Score 1095; DB 3; Length 248;
Best Local Similarity 92.1%; Pred. No. 3.9e-119;
Matches 211; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 2 ALVATGNDTTKPDLYLKNSEAINSLALPPPAVGSIAFLNDQAMTEQGLLNTERG 61
DB 20 ALVAGNDATTKPDLYLKNQAIDSLALPPPEVGSIAFLNDQAMTEKGLLNTERG 79
QY 62 KLAEDANLSSGVANAFSSAFSGSPITEKDAPOHLKLLTNMIEDAGDLATRSADHYMRI 121
DB 80 KLAEDANLSSGVANAFSSAFSGSPITEKDAPOHLKLLTNMIEDAGDLATRSADHYMRI 139
QY 122 RPFAPYGVSTCNTTEODKLSKNGSYPSGHTSIGMATLVLAELNIPORONEILKRGYELGQ 181
DB 140 RPFAPYGVSTCNTTEODKLSKNGSYPSGHTSIGMATLVLAELNIPORONEILKRGYELGQ 199
QY 182 SRVIGYHWSQDVDAARVGSAAVATLHTNPAFOOOLQAKAEPAKHOK 230
DB 200 SRVIGYHWSQDVDAARVGSAAVATLHTNPAFOOOLQAKAEPAKHOK 248

RESULT 13
US-09-727-578-24
Sequence 24, Application US/09727578
Patent No. 6355472
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/727,578
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Enterobacter aerogenes
STRAIN: IFO 12010
US-09-727-578-24

Query Match 92.0%; Score 1095; DB 3; Length 248;
Best Local Similarity 92.1%; Pred. No. 3.9e-119;
Matches 211; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 2 ALVATGNDTTKPDLYLKNSEAINSLALPPPAVGSIAFLNDQAMTEQGLLNTERG 61
DB 20 ALVAGNDATTKPDLYLKNQAIDSLALPPPEVGSIAFLNDQAMTEKGLLNTERG 79
QY 62 KLAEDANLSSGVANAFSSAFSGSPITEKDAPOHLKLLTNMIEDAGDLATRSADHYMRI 121
DB 80 KLAEDANLSSGVANAFSSAFSGSPITEKDAPOHLKLLTNMIEDAGDLATRSADHYMRI 139
QY 122 RPFAPYGVSTCNTTEODKLSKNGSYPSGHTSIGMATLVLAELNIPORONEILKRGYELGQ 181
DB 140 RPFAPYGVSTCNTTEODKLSKNGSYPSGHTSIGMATLVLAELNIPORONEILKRGYELGQ 199
QY 182 SRVIGYHWSQDVDAARVGSAAVATLHTNPAFOOOLQAKAEPAKHOK 230
DB 200 SRVIGYHWSQDVDAARVGSAAVATLHTNPAFOOOLQAKAEPAKHOK 248

RESULT 14
US-08-750-145A-22
Sequence 22, Application US/08750145A
Patent No. 6010851
GENERAL INFORMATION:
APPLICANT: MIHARA, Yasuhiro
APPLICANT: UTAGAWA, Takashi
APPLICANT: YAMADA, Hideaki
APPLICANT: ASANO, Yasuhisa
TITLE OF INVENTION: Method for Producing Nucleoside-5'-
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFF. DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,145A
FILING DATE: 01-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-149781
FILING DATE: 05-May-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-094680
FILING DATE: 26-Mar-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0830-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Klebsiella planticola
STRAIN: IFO 14939
US-08-750-145A-22

Query Match 90.8%; Score 1080; DB 3; Length 248;
Best Local Similarity 90.8%; Pred. No. 2.2e-117;
Matches 208; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 2 ALVATGNDTTTKPDLYLKNSSEAINSLALPPPPAVGSIAPLNDQAWYEQRLRLRTERG 61
DB 20 ALVPAAGNDATTTKPDLYLKNAQALDSIALLPPEVSGIAPLNDQAWYEQRLRLRTERG 79
QY 62 KLAEDANLSSGGVANAFAFGSPITEKDPALHKLITNMIEDAGDLATRSADHYMRI 121
DB 80 KLAEDANLSAGGVANAFSAFGSPISEKDPALHKLITNMIEDAGDLATRSADHYMRI 139
QY 122 RPPAFYGVSTCNTTEODKLSNGSYPSGHTSIGMATLVLAETNPORONEILKRGYELGQ 181
DB 140 RPPAFYGVSTCNTTEODKLSNGSYPSGHTSIGMATLVLAETNPORONEILKRGYELG 199
QY 182 SRVTCGYHMOQSDVDAAVVGSAVVATLHTNPAFQOOLQKAKAEPAHQK 230
DB 200 SRVTCGYHMOQSDVDAAVVGSAVVATLHTNPAFQOOLQKAKAEPAHQK 248

RESULT 15

US-08-975-698A-26
Sequence 26, Application US/08975698A
Patent No. 6015697

GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:

ADDRESSES: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,698A

FILING DATE: 21-NOV-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 0010-0885-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:

ORGANISM: Klebsiella planticola
STRAIN: IFO 14939
US-08-975-698A-26

Query Match 90.8%; Score 1080; DB 3; Length 248;
Best Local Similarity 90.8%; Pred. No. 2.2e-117;
Matches 208; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 2 ALVATGNDTTTKPDLYLKNSSEAINSLALPPPPAVGSIAPLNDQAWYEQRLRLRTERG 61
DB 20 ALVPAAGNDATTTKPDLYLKNAQALDSIALLPPEVSGIAPLNDQAWYEQRLRLRTERG 79
QY 62 KLAEDANLSSGGVANAFAFGSPITEKDPALHKLITNMIEDAGDLATRSADHYMRI 121
DB 80 KLAEDANLSAGGVANAFSAFGSPISEKDPALHKLITNMIEDAGDLATRSADHYMRI 139
QY 122 RPPAFYGVSTCNTTEODKLSNGSYPSGHTSIGMATLVLAETNPORONEILKRGYELGQ 181
DB 140 RPPAFYGVSTCNTTEODKLSNGSYPSGHTSIGMATLVLAETNPORONEILKRGYELG 199
QY 182 SRVTCGYHMOQSDVDAAVVGSAVVATLHTNPAFQOOLQKAKAEPAHQK 230
DB 200 SRVTCGYHMOQSDVDAAVVGSAVVATLHTNPAFQOOLQKAKAEPAHQK 248

Search completed: March 2, 2005, 20:28:50
Job time : 31.1961 secs

TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Escherichia blattae
STRAIN: JCM 1650
US-09-727-578-6

Query Match 100.0%; Score 1190; DB 9; Length 231;
Best Local Similarity 100.0%; Pred. No. 1.5e-117;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSIAFLNDQMYEQGRLNTER 60
DB 1 LALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSIAFLNDQMYEQGRLNTER 60
QY 61 GKLAEDANLSSGGVANAFAFGSPITEKAPALHKLNTMIEDAGDLATRSKDHMYR 120
DB 61 GKLAEDANLSSGGVANAFAFGSPITEKAPALHKLNTMIEDAGDLATRSKDHMYR 120
QY 121 IRPFAFYGVSTCNTTEODKLSKNGSYPSGHTSIGMATALVLAETNPORONEILKRGYELG 180
DB 121 IRPFAFYGVSTCNTTEODKLSKNGSYPSGHTSIGMATALVLAETNPORONEILKRGYELG 180
QY 181 QSRVTCGYHWSQVDARVGSAAVATLTNPFAFQQLQKAKAFQHQK 231
DB 181 QSRVTCGYHWSQVDARVGSAAVATLTNPFAFQQLQKAKAFQHQK 231

RESULT 2
US-09-727-578-7
Sequence 7, Application US/09727578
Publication No. US20020004590A1
GENERAL INFORMATION:

APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/727,578
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Escherichia blattae
STRAIN: JCM 1650
US-09-727-578-7

Query Match 100.0%; Score 1190; DB 9; Length 249;
Best Local Similarity 100.0%; Pred. No. 1.7e-117;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSIAFLNDQMYEQGRLNTER 60
DB 19 LALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSIAFLNDQMYEQGRLNTER 78
QY 61 GKLAEDANLSSGGVANAFAFGSPITEKAPALHKLNTMIEDAGDLATRSKDHMYR 120
DB 79 GKLAEDANLSSGGVANAFAFGSPITEKAPALHKLNTMIEDAGDLATRSKDHMYR 138
QY 121 IRPFAFYGVSTCNTTEODKLSKNGSYPSGHTSIGMATALVLAETNPORONEILKRGYELG 180
DB 139 IRPFAFYGVSTCNTTEODKLSKNGSYPSGHTSIGMATALVLAETNPORONEILKRGYELG 180
QY 181 QSRVTCGYHWSQVDARVGSAAVATLTNPFAFQQLQKAKAFQHQK 231
DB 199 QSRVTCGYHWSQVDARVGSAAVATLTNPFAFQQLQKAKAFQHQK 249

RESULT 3
US-09-727-578-24

Sequence 24, Application US/09727578
Publication No. US20020004590A1
GENERAL INFORMATION:

APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/727,578
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Enterobacter aerogenes
STRAIN: IFO 12010
US-09-727-578-24

Query Match 92.0%; Score 1095; DB 9; Length 248;
Best Local Similarity 92.1%; Pred. No. 26-107;
Matches 211; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 2 ALVATGNDTTKPPDYLYKNSEAINSLALPPPAVGSIAFLNDQAMTEQGRLLNTERG 61
DB 20 ALVPAQNDAITKPPDYLYKNQAIDSLALPPPEVGSIAFLNDQAMTEKGRLLNTERG 79
QY 62 KLAADANLSSGVANAFSGAFSPITEKDA PALHKLNTMIEDAGDLATRSADHYMRI 121
DB 80 KLAADANLSSGVANAFSGAFSPITEKDA PALHKLNTMIEDAGDLATRSADHYMRI 139
QY 122 RPFAYGVSTCNTTEODKLSKNGSPSGHTSIGMATLVLAELNFORONEILKRGYEIGE 181
DB 140 RPFAYGVSTCNTTEODKLSKNGSPSGHTSIGMATLVLAELNFORONEILKRGYEIGE 199
QY 182 SRVIGYHWSQDVAARVGSAAVATLHTNPAFOOQLOKAKAEPAQHOK 230
DB 200 SRVIGYHWSQDVAARVGSAAVATLHTNPAFOOQLOKAKAEPAKHOK 248

RESULT 4
US-09-727-578-26
Sequence 26, Application US/09727578
Publication No. US20020004590A1

GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/727,578
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:

ORGANISM: Klebsiella planticola
STRAIN: IFO 14939
US-09-727-578-26

Query Match 90.8%; Score 1080; DB 9; Length 248;
Best Local Similarity 90.8%; Pred. No. 7,7e-106;
Matches 208; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 2 ALVATGNDTTKPPDYLYKNSEAINSLALPPPAVGSIAFLNDQAMTEQGRLLNTERG 61
DB 20 ALVPAQNDAITKPPDYLYKNQAIDSLALPPPEVGSIAFLNDQAMTEKGRLLNTERG 79
QY 62 KLAADANLSSGVANAFSGAFSPITEKDA PALHKLNTMIEDAGDLATRSADHYMRI 121
DB 80 KLAADANLSSGVANAFSGAFSPITEKDA PALHKLNTMIEDAGDLATRSADHYMRI 139
QY 122 RPFAYGVSTCNTTEODKLSKNGSPSGHTSIGMATLVLAELNFORONEILKRGYEIGE 181
DB 140 RPFAYGVSTCNTTEODKLSKNGSPSGHTSIGMATLVLAELNFORONEILKRGYEIGE 199
QY 182 SRVIGYHWSQDVAARVGSAAVATLHTNPAFOOQLOKAKAEPAQHOK 230
DB 200 SRVIGYHWSQDVAARVGSAAVATLHTNPAFOOQLOKAKAEPAKHOK 248

RESULT 5
US-09-727-578-22
Sequence 22, Application US/09727578
Publication No. US20020004590A1

GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/727,578
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE: Providencia stuartii
STRAIN: ATCC 29851
US-09-727-578-22

Query Match 82.9%; Score 986; DB 9; Length 248;
Best Local Similarity 81.2%; Pred. No. 7.2e-96;
Matches 186; Conservative 24; Mismatches 19; Indels 0; Gaps 0;

QY 2 ALVATGNDTTKPDLYLKNSSEAINSLALPPPPAVGSIAPLNDQAMEYEGRLNTERG 61
DB 20 AAIPEGNDATTKPDLYLKNSQALDSLALPPPEVGSIFLNDQAMEYEGRLNTERG 79
QY 62 KLAEDANLSSGGVANAFAFGSPITEKDPALHKLITNMIEDAGDLATRSADHYMR 121
DB 80 EQAKADADLAAGVANAFAFGSPITEKDPALHKLITNMIEDAGDLATRSADHYMR 139
QY 122 RPPAFYGVSTCNTTEODKLSKNGSPSGHTSIGWATLVLAETINPORONEILRGYELG 181
DB 140 RPPAFYGVATCNTKQDKLSKNGSPSGHTSIGWATLVLAETINPORONEILRGYELG 199
QY 182 SRVTCGYHMOSDVDAARIVGSAVAATLTHTNPAFOOQLKAKAEPAHQK 230
DB 200 SRVTCGYHMOSDVDAARIVGSAVAATLTHTNPAFOOQLKAKAEPAHQK 248

RESULT 6
US-09-727-578-3
; Sequence 3, Application US/09727578
; Publication No. US2002004590A1
; GENERAL INFORMATION:
; APPLICANT: MIHARA, YASUHIRO
; APPLICANT: UYAGAWA, TAKASHI
; APPLICANT: YAMADA, HIDEAKI
; APPLICANT: ASANO, YASUHIISA
; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P. C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/727,578
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/975,698
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0010-0885-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO. 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 249 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Morganella morganii
; STRAIN: NCIMB 10466
; US-09-727-578-3

Query Match 81.4%; Score 969; DB 9; Length 249;
Best Local Similarity 79.2%; Pred. No. 4.6e-94;

Matches 183; Conservative 20; Mismatches 28; Indels 0; Gaps 0;

QY 1 LALVATGNDTTKPDLYLKNSSEAINSLALPPPPAVGSIAPLNDQAMEYEGRLNTER 60
DB 19 LAAIPEGNDATTKPDLYLKNSQALDSLALPPPEVGSIFLNDQAMEYEGRLNTER 78
QY 61 KLAEDANLSSGGVANAFAFGSPITEKDPALHKLITNMIEDAGDLATRSADHYMR 120
DB 79 GKAQADADLAAGVANAFAFGSPITEKDPALHKLITNMIEDAGDLATRSADHYMR 138
QY 121 RPPAFYGVSTCNTTEODKLSKNGSPSGHTSIGWATLVLAETINPORONEILRGYELG 180
DB 139 RPPAFYGVETCNTKQDKLSKNGSPSGHTSIGWATLVLAETINPORONEILRGYELG 198
QY 181 SRVTCGYHMOSDVDAARIVGSAVAATLTHTNPAFOOQLKAKAEPAHQK 231
DB 199 SRVTCGYHMOSDVDAARIVGSAVAATLTHTNPAFOOQLKAKAEPAHQK 249

RESULT 7
US-10-220-481-116
; Sequence 116, Application US/10220481
; Publication No. US20040110670A1
; GENERAL INFORMATION:
; APPLICANT: ARICO, Maria B., et al.
; TITLE OF INVENTION: Heterologous Expression of Neisserial Proteins
; FILE REFERENCE: CHIR-15883/01US
; CURRENT APPLICATION NUMBER: US/10/220,481
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: PCT/IB01/00452
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 633
; SOFTWARE: Seqwin99, version 1.02
; SEQ ID NO 116
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Novel protein
; US-10-220-481-116

Query Match 81.1%; Score 965; DB 16; Length 249;
Best Local Similarity 79.1%; Pred. No. 1.2e-93;
Matches 182; Conservative 20; Mismatches 28; Indels 0; Gaps 0;

QY 2 ALVATGNDTTKPDLYLKNSSEAINSLALPPPPAVGSIAPLNDQAMEYEGRLNTERG 61
DB 20 AAIPEGNDATTKPDLYLKNSQALDSLALPPPEVGSIFLNDQAMEYEGRLNTERG 79
QY 62 KLAEDANLSSGGVANAFAFGSPITEKDPALHKLITNMIEDAGDLATRSADHYMR 121
DB 80 KQAQADADLAAGVANAFAFGSPITEKDPALHKLITNMIEDAGDLATRSADHYMR 139
QY 122 RPPAFYGVSTCNTTEODKLSKNGSPSGHTSIGWATLVLAETINPORONEILRGYELG 181
DB 140 RPPAFYGVETCNTKQDKLSKNGSPSGHTSIGWATLVLAETINPORONEILRGYELG 199
QY 182 SRVTCGYHMOSDVDAARIVGSAVAATLTHTNPAFOOQLKAKAEPAHQK 231
DB 200 SRVTCGYHMOSDVDAARIVGSAVAATLTHTNPAFOOQLKAKAEPAHQK 249

RESULT 8
US-09-727-578-4
; Sequence 4, Application US/09727578
; Publication No. US2002004590A1
; GENERAL INFORMATION:
; APPLICANT: MIHARA, YASUHIRO
; APPLICANT: UYAGAWA, TAKASHI
; APPLICANT: YAMADA, HIDEAKI
; APPLICANT: ASANO, YASUHIISA
; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
; TITLE OF INVENTION: ESTER

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;
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT, P. C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/727,578
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/975,698
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0010-0885-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Morganella morganii
; STRAIN: NCTIMB 10466
; US-09-727-578-4
;
Query Match 80.8%; Score 962; DB 9; Length 229;
Best Local Similarity 79.4%; Pred. No. 2.3e-93;
Matches 181; Conservative 20; Mismatches 27; Indels 0; Gaps 0;
;
Qy 4 VATGDTTTPDLYYLNKSEAINSLALLPPRPVAGSIAPLNDQAMYEQRLNTERGKL 63
Db 2 IPAGDATTTPDLYYLNKSEAINSLALLPPRPVAGSIAPLNDQAMYEQRLNTERGKL 61
Qy 64 AADANLSSGGVANAFCGSPITEKDPALHKLNTNMIEDAGDLATRSADHYMRIRP 123
Db 62 AOADADLAAGVATAFSGAFGYPIREKDSPELYKLLTNMIEDAGDLATRSADHYMRIRP 121
Qy 124 FAFYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLAELNPPORONELIKRGYELGQSR 183
Db 122 FAFYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLAELNPPORONELIKRGYELGQSR 181
Qy 184 VICGYHMOGDVDAARVGSAAVATLHTNPAFOOOLOKAKAEFAQOKK 231
Db 182 VICGYHMOGDVDAARVGSAAVATLHTNPAFOOOLOKAKAEFAQOKK 229
;
RESULT 9
US-09-727-578-28
; Sequence 28, Application US/09727578
; Publication No. US20020004590A1
; GENERAL INFORMATION:
; APPLICANT: MIHARA, YASUHIRO
; APPLICANT: UTAGAWA, TAKASHI
; APPLICANT: YAMADA, HIDEAKI
; APPLICANT: ASANO, YASUHIISA
; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
; TITLE OF INVENTION: ESTER
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT, P. C.
```

```

;
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/727,578
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/975,698
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0010-0885-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 244 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Serratia ficaria
; STRAIN: IAM 13540
; US-09-727-578-28
;
Query Match 64.5%; Score 768; DB 9; Length 244;
Best Local Similarity 66.8%; Pred. No. 9.4e-73;
Matches 145; Conservative 29; Mismatches 43; Indels 0; Gaps 0;
;
Qy 9 DTTTKPDLYYLNKSEAINSLALLPPRPVAGSIAPLNDQAMYEQRLNTERGKL 68
Db 23 DVTTHPEVYFLQESQSIDSLALLPPPPMDSIDFLNDKAYDAGKIVNTTRGKQAYDA 82
Qy 69 NLSSGCVANAFSGAFSGSPITEKDPALHKLNTNMIEDAGDLATRSADHYMRIRP 128
Db 83 HVAAGGVAAAFSNAFGEIAQKTPPELFLVWKREKEDAGDLATRSADHYMRIRP 142
Qy 129 VSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLAELNPPORONELIKRGYELGQSR 188
Db 143 EATCRPDESESTLSKNGSYPSGHTTIGWATLVLAELNPPARQGEILRGYDMGQSRVIGY 202
Qy 189 HMOSDVTDAARVGSAAVATLHTNPAFOOOLOKAKAEF 225
Db 203 HMOSDVTDAARVGSAAVATLHTNPAFOOOLOKAKAEF 239
;
RESULT 10
US-09-738-626-4817
; Sequence 4817, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
```

;; CURRENT APPLICATION NUMBER: US/09/738,626
;; CURRENT FILING DATE: 2000-12-18
;; PRIOR APPLICATION NUMBER: JP 99/377484
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: JP 00/159162
;; PRIOR FILING DATE: 2000-04-07
;; PRIOR APPLICATION NUMBER: JP 00/280988
;; PRIOR FILING DATE: 2000-08-03
;; NUMBER OF SEQ ID NOS: 7059
;; SOFTWARE: PatentIn ver. 3.0
;; SEQ ID NO 4817
;; LENGTH: 622
;; TYPE: PRT
;; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4817

Query Match 12.0%; Score 143; DB 9; Length 622;
Best Local Similarity 27.4%; Pred. No. 7.4e-06;
Matches 49; Conservative 24; Mismatches 72; Indels 34; Gaps 6;

QY 65 AEDANLSSGGVANA-----FSGAFSGPTEKDPALHLLTNMTEDAGDLATRSKXHYMR 120
DB 159 ATTKYNDGNGVNNMNAETGELGISTVDLIEAIRQHATSN-----NAKAYXY 207
QY 121 IRPPAF-----YGVST---CNTTED--KLSKNGSPSGHTSIGWATALVLAETIN 165
DB 208 PRPRWTESIEPEAMGRGVMPPEYANPLRKDESEASDGGFSGHTSAGMATNGLAAYAF 267
QY 166 PORNEILIKRGYELGOSRVTCGYHMOQSDVDAAVGSAAVATITHTPAQOOLQKAAE 224
DB 268 PQQYDKLMTAAIGESRIQLGMHSLPUDVIGGRVLTATTAALNDP-----NLDVYKAE 322

RESULT 11
US-10-437-963-165801
;; Sequence 165801, Application US/10437963
;; Publication No. US20040123343A1
;; GENERAL INFORMATION:
;; APPLICANT: La Rosa, Thomas J.
;; APPLICANT: Kovalic, David K.
;; APPLICANT: Zhou, Yihua
;; APPLICANT: Cao, Yongwei
;; APPLICANT: Wu, Wei
;; APPLICANT: Boukharov, Andrey A.
;; APPLICANT: Barbazuk, Brad
;; APPLICANT: Li, Ping
;; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
;; FILE REFERENCE: 38-21(53221)B
;; CURRENT APPLICATION NUMBER: US/10/437,963
;; CURRENT FILING DATE: 2003-05-14
;; NUMBER OF SEQ ID NOS: 204966
;; SEQ ID NO 165801
;; LENGTH: 414
;; TYPE: PRT
;; ORGANISM: Oryza sativa
;; FEATURE:
;; OTHER INFORMATION: Clone ID: PAT_WRT4530_64572C.1.dep
US-10-437-963-165801

Query Match 9.2%; Score 109; DB 16; Length 414;
Best Local Similarity 26.1%; Pred. No. 0.016;
Matches 58; Conservative 33; Mismatches 75; Indels 56; Gaps 12;

QY 2 ALVATGNTTTRKPDLYIAKSEAINSLALPPRAVGSIAFLNDQAMYEGRLLRNTERG 61
DB 68 AVAAPDDDDGNP-----LGGAMKHMALAPPSPSKSKKXNSNVWTR-----PNSRKG 117
QY 62 -KLAEDANLSSGGVANA-----FSGAFSGPIT-----EKDAPALHLLTNMT-- 102
DB 118 KKKAKQANALAGSAGANGRLPKFSGDDDELVTTPRAAEKNDADLPVLLSVFK 177
QY 103 ---IEDAGDLATRSKXHYMRIRPFAYGVSTCNTTEQDKLSKNGSPSGHTSIGMAT-- 157

DB 178 SPRVEYSDRLTAGSRKGRMR--ATRGVAAGANYFEVKYLAHLS--TGHTRIGMATNN 233
QY 158 ALVLAETINPORNEILIKRGYELGOSRVTCGYHMOQSDVDAARV 199
DB 234 ADIHAFV-----GYD-----VFGFGYR-DMGDKTV 257

RESULT 12
US-10-374-780A-1704
;; Sequence 1704, Application US/10374780A
;; Publication No. US20040019927A1
;; GENERAL INFORMATION:
;; APPLICANT: Sherman, Bradley K
;; APPLICANT: Riechmann, Jose Luis
;; APPLICANT: Jiang, Cai-zhong
;; APPLICANT: Heard, Jacqueline E
;; APPLICANT: Haake, Volker
;; APPLICANT: Creelman, Robert A
;; APPLICANT: Ratcliffe, Oliver
;; APPLICANT: Adam, Luc J
;; APPLICANT: Reuber, T. Lynne
;; APPLICANT: Keddie, James
;; APPLICANT: Brown, Pierre E
;; APPLICANT: Pilgrim, Marsha L
;; APPLICANT: Dubeil III, Arnold T
;; APPLICANT: Pineda, Omaira
;; APPLICANT: Yu, Guo-Liang
;; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
;; FILE REFERENCE: MBI-0047 CIP
;; CURRENT APPLICATION NUMBER: US/10/374,780A
;; PRIOR FILING DATE: 2003-02-25
;; PRIOR APPLICATION NUMBER: 09/837,944
;; PRIOR FILING DATE: 2001-04-18
;; PRIOR APPLICATION NUMBER: 60/310,847
;; PRIOR FILING DATE: 2001-08-09
;; PRIOR APPLICATION NUMBER: 09/934,455
;; PRIOR FILING DATE: 2001-08-22
;; PRIOR APPLICATION NUMBER: 60/336,049
;; PRIOR FILING DATE: 2001-11-19
;; PRIOR APPLICATION NUMBER: 60/338,692
;; PRIOR FILING DATE: 2001-12-11
;; PRIOR APPLICATION NUMBER: 10/171,468
;; PRIOR FILING DATE: 2002-06-14
;; PRIOR APPLICATION NUMBER: 10/225,066
;; PRIOR FILING DATE: 2002-08-09
;; PRIOR APPLICATION NUMBER: 10/225,067
;; PRIOR FILING DATE: 2002-08-09
;; PRIOR APPLICATION NUMBER: 10/225,068
;; PRIOR FILING DATE: 2002-08-09
;; NUMBER OF SEQ ID NOS: 2906
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 1704
;; LENGTH: 353
;; TYPE: PRT
;; ORGANISM: Oryza sativa
;; FEATURE:
;; OTHER INFORMATION: Orthologous to G1652
US-10-374-780A-1704

Query Match 8.4%; Score 99.5; DB 15; Length 353;
Best Local Similarity 24.5%; Pred. No. 0.13;
Matches 63; Conservative 31; Mismatches 92; Indels 71; Gaps 13;

QY 23 BAINSIALP--PPRAVGSIAFLNDQAMYEGRLLRNT--TERGKLAED-----AN 69
DB 13 ETLQHLHPLPATPPRAGGYA--GDNATPFLQALRESSVQNGMAPEPTAHRGHRASN 70
QY 70 LSSGVANAFAFGSPITEKDA-----PALHKLITNMTED 105
DB 71 SWSSGDTDSVSGGGGAVMEHDSSTPSNVRCAAGGGGGGGGLFVSNFSSANTOP 130
QY 106 AGDLATRSKXHYMRIRPFAYG-----VSTCNTTEQDKLSK--NGSPSGHTSI 153

Db 131 CNDQATPSNPPTTTRAR----YGGGVRVYLPAAVSPSPGQRRRRASSKNGGGSSSA 186
 Oy 154 G-WATLALVLAETINPQROHEILKRGVLEGSRYICGYHMOSDVDAARVGSANVALTLHNP 212
 Db 187 APYAEHIIAE--RRRKRINQRIEL--STVIFGL---KKMDKATILSDAV----- 231
 Oy 213 AFOOOLQAKAEFAOHQ 229
 Db 232 RYVKEMQEKLSLEOHQ 248

RESULT 13

US-10-437-963-194124
 ; Sequence 194124, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 194124
 ; LENGTH: 353
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_90197C.1.pcp
 ; US-10-437-963-194124

Query Match 8.4%; Score 99.5; DB 16; Length 353;
 Best Local Similarity 24.5%; Pred. No. 0.13;
 Matches 63; Conservative 31; Mismatches 92; Indels 71; Gaps 13;
 Oy 23 EAINSLALLP--PPAVGSIAFLNDQAWYEGRLRN---TERGLAED-----AN 69
 Db 13 ETLQHLPLPATPPAGGYA--GNATPPIQLRESSVSONGMAPEPTAHGHRASN 70
 Oy 70 LSSGCVANAFSGAFSPITEKDA-----PALHKLITNMTD 105
 Db 71 SMSGSDTDSVSGGGGAVMEHDMSTSPNSVRCACAGGGGGGGLMFPVSNMFPSSAMQP 130
 Oy 106 AGDLATRSADKHVIRPPAYG-----VSTCNTTEODKLSK--NGSYPSGHTSI 153
 Db 131 CNDQATPSNPPTTTRAR----YGGGVRVYLPAAVSPSPGQRRRRASSKNGGGSSSA 186
 Oy 154 G-WATLALVLAETINPQROHEILKRGVLEGSRYICGYHMOSDVDAARVGSANVALTLHNP 212
 Db 187 APYAEHIIAE--RRRKRINQRIEL--STVIFGL---KKMDKATILSDAV----- 231
 Oy 213 AFOOOLQAKAEFAOHQ 229
 Db 232 RYVKEMQEKLSLEOHQ 248

RESULT 14

US-10-282-122A-77490
 ; Sequence 77490, Application US/10282122A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Hasebeck, Robert

APPLICANT: Ohlsen, Kari
 APPLICANT: Zykand, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forsyth, R.
 APPLICANT: Xu, H.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: EUTRA.034A
 ; CURRENT APPLICATION NUMBER: US/10/282,122A
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/230,335
 ; PRIOR FILING DATE: 2000-09-06
 ; PRIOR APPLICATION NUMBER: 60/230,347
 ; PRIOR FILING DATE: 2000-09-09
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/267,636
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 78614
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 77490
 ; LENGTH: 178
 ; TYPE: PRT
 ; ORGANISM: Vibrio cholerae
 ; US-10-282-122A-77490

Query Match 8.1%; Score 96; DB 15; Length 178;
 Best Local Similarity 31.0%; Pred. No. 0.11;
 Matches 27; Conservative 14; Mismatches 42; Indels 4; Gaps 1;
 Oy 115 KDHVIRPPAFYGVSTCNTTEODKLSKNGSYPSGHTSIGWATLVAETINPQROHEILK 174
 Db 81 KNSFORRRPQELSLVTAIYTPSDRY---SLPSGHTAAAFVWATLIGYIFHWYAVALC 136
 Oy 175 RGYELGOSRYICGYHMOSDVDAARVVG 201
 Db 137 WAGLIGLARVILGVHPLSDVTAAGALIG 163

RESULT 15

US-10-437-963-122794
 ; Sequence 122794, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966

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OM protein - protein search, using sw model

Run on: March 2, 2005, 20:15:51 ; Search time 25.6667 Seconds
(without alignments)
865.951 Million cell updates/sec

Title: US-09-807-990A-124

Sequence: 1 LAVALTGNDTTKPDLYLK.....PAFGQQLQKAKAFPAQHOKK 231

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	986	82.9	248	1	PROFCS acid phosphatase (
2	969	81.4	249	1	acid phosphatase (
3	485	40.8	250	1	acid phosphatase (
4	477	40.1	250	1	acid phosphatase (
5	329	27.6	264	1	acid phosphatase (
6	274.5	23.1	258	2	acid phosphatase (
7	189.5	15.9	2314	2	hypothetical prote
8	172.5	14.5	241	2	probable acid phos
9	157	13.2	591	2	uncharacterized pr
10	141	11.8	660	2	serine proteinase
11	141	11.8	660	2	vanadium chlorop
12	105	8.8	145	2	conserved hypotet
13	99.5	8.4	259	2	protein B0205.3 (i
14	96	8.1	178	2	hypothetical prote
15	93	7.8	608	2	conserved hypotet
16	91	7.6	217	2	hypothetical prote
17	91	7.6	242	2	conserved hypotet
18	90.5	7.6	437	2	hypothetical prote
19	89.5	7.5	1157	2	PAS1 protein - yea
20	88.5	7.4	589	2	ATP-dependent heli
21	88	7.4	589	2	hypothetical prote
22	87.5	7.4	320	2	hypothetical prote
23	86.5	7.3	368	2	probable porin Vcl
24	86.5	7.3	824	2	helicase, ATP-depe
25	86.5	7.3	824	2	ATP-dependent heli
26	86	7.2	292	2	phosphatidylglycer
27	85.5	7.2	390	2	2-C-methyl-D-erythr
28	85	7.1	725	2	vach-like (shigell
29	85	7.1	766	2	P element transpos

30	84	7.1	474	2	AE3426
31	84	7.1	2004	2	P95133
32	83	7.0	548	2	AC0871
33	83	7.0	753	2	S22802
34	83	7.0	1588	2	A86036
35	83	7.0	1588	2	H91188
36	82.5	6.9	525	2	C62914
37	82.5	6.9	561	1	VGN241
38	82.5	6.9	921	2	A54139
39	82	6.9	562	2	S46281
40	81	6.8	247	2	T35796
41	81	6.8	490	2	S75539
42	81	6.8	726	2	D97012
43	80.5	6.8	218	2	E97497
44	80.5	6.8	218	2	AB2716
45	80.5	6.8	272	1	G82076

ALIGNMENTS

RESULT 1
acid phosphatase (EC 3.1.3.2) - Providencia stuartii
C:Species: Providencia stuartii
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C:Accession: S19888
R:Riccio, M.L.; Lombardi, G.; Chiesurin, A.; Satta, G.
Submitted to the EMBL Data Library, February 1992
A:Reference number: S19888
A:Accession: S19888
A:Molecule type: DNA
A:Residues: 1-248 <RIC>
A:Cross-references: UNIPROT:P26975; EMBL:X64820; NID:945861; PIDN:CAA46032.1; PID:945862
C:Genetics:
A:Gene: phoN
C:Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic do
C:Keywords: phosphoric monoster hydrolase
F:103-222/Domain: glucose-6-phosphatase catalytic domain homology <GRH>

Query Match 82.9%; Score 986; DB 1; Length 248;
Best Local Similarity 81.2%; Pred. No. 4.5e-80;
Matches 186; Conservative 24; Mismatches 19; Indels 0; Gaps 0;

QY	2	ALVATGNDTTKPDLYLKNSSEAINSLALPPPAVGSIAFLNDQAMYEQGRLLNTERG	61
DB	20	AAIPGNDVTTKPDLYLKNSQAIDSLALPPPEVGSILFLNDQAMYEKRLNTERG	79
QY	62	KLAEDANLSSGVANAFSGAFSPITEKDA PALHKLITNMIEDAGDLATRSADHYMRI	121
DB	80	EQAKADNLAAGVANAFSEAFGPIITEKDAPEIHKLTITNIEDAGDLATRSADHYMRI	139
QY	122	RPAFYGVSTNTTEODLSTNGSGYPSGHTSIGVATLVLAENIPORQNEILKGYELGQ	181
DB	140	RPAFYGVATCNTDQDLSTNGSGYPSGHTSIGVATLVLAENIPORQNEILKGYELGQ	199
QY	182	SRVTCGYHWDSDVDAARVYSAVATLTHTNPAFQQLQKAKAFPAQHOKK	230
DB	200	SRVTCGYHWDSDVDAARIVASGAVALTSHNPEFOKLOKADFEPAKLKK	248

RESULT 2
S19187:
acid phosphatase (EC 3.1.3.2) - Morganella morganii
C:Species: Morganella morganii
C:Date: 28-Jan-2000 #sequence_revision 28-Jan-2000 #text_change 09-Jul-2004
C:Accession: S19187
R:Thaller, M.C.; Berluti, F.; Schipka, S.; Rosolini, G.M.
Submitted to the EMBL Data Library, February 1992
A:Description: Sequencing the Morganella morganii phoC gene coding for a periplasmic ac
A:Reference number: S19187
A:Accession: S19187
A:Molecule type: DNA

A;Residues: 1-249 <THA>
 A;Cross-references: UNIPROT:P28501; EMBL:X64444; NID:G44463; PID:CAA45774.1; PID:G44464
 C;Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic dc
 C;Keywords: phosphoric monoester hydrolase
 F;109-222/Domain: glucose-6-phosphatase catalytic domain homology <GPH>

Query Match

Best Local Similarity 81.4%; Score 969; DB 1; Length 249;
 Matches 183; Conservative 20; Mismatches 28; Indels 0; Gaps 0;

Qy 1 LALVNTGNDTTKPLDYLYKNSDAINSLALPPPAVGSIAPLNDQAMYEQGRLLRTER 60
 Db 19 LPAIPAGNDATTPDYLYLKNEQADSLKLPPEPVSGISQFLNDQAMYEGRLLRTER 78
 Qy 61 GTLAEDANLSSGGVANAFAFGSPITEKDAAPALHKLITNMIEDAGLATRSKADHYMR 120
 Db 79 GKQADADLAAGVATFSGAFGPIREKDSPELYKLLINMIDADGLATRSKADHYMR 138
 Qy 121 IRPFAFYGVSTCTTEQDKLSKNGSGPSGHTSIGMATLVLAELNIPORNEILKGYELG 180
 Db 139 IRPFAFYGVSTCTTEQDKLSKNGSGPSGHTSIGMATLVLAELNIPORNEILKGYELG 198
 Qy 181 QSRVIGCYHMQSDVDAARVGSAAVATLHTNPAFOQLQAKAEFAQHK 231
 Db 199 QSRVIGCYHMQSDVDAARVGSAAVATLHTNPAFOQLQAKAEFAQHK 249

RESULT 3

A41330
 acid phosphatase (EC 3.1.3.2) Phos precursor - Salmonella typhimurium
 N;Alternate names: glycerophosphatase, nonspecific acid phosphatase; phosphomonoesterase
 C;Species: Salmonella typhimurium
 C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
 A;Accession: S20958; A41330; S14515; S18926
 R;Goleman, E.A.; Sater, U.; M.H.; Ochman, H.
 EMBL J. 11, 1309-1316, 1992
 A;Title: Horizontal transfer of a phosphatase gene as evidence for mosaic structure of
 A;Reference number: S20958; MUID:9224869; PMID:1339343
 A;Accession: S20958
 A;Molecule type: DNA
 A;Residues: 1-250 <GRO>
 A;Cross-references: UNIPROT:P26976; EMBL:X63599; NID:G47823; PID:CAA45144.1; PID:G47824
 R;Kasahara, M.; Nakata, A.; Shingawa, H.
 J. Bacteriol. 173, 6760-6765, 1991
 A;Title: Molecular analysis of the Salmonella typhimurium pho gene, which encodes nonsp
 A;Reference number: A41330; MUID:92041557; PMID:1938882
 A;Accession: A41330
 A;Molecule type: DNA
 A;Residues: 1-228 'SVRS' <KAS>
 A;Cross-references: GB:X59036; NID:G48894; PID:CAA41760.1; PID:G48895
 C;Genetics:
 A;Gene: phoN
 A;Map position: 96 min
 A;Note: regulated by the two-component regulatory system consisting of phoP and phoQ
 C;Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic dc
 C;Keywords: periplasmic space; phosphoric monoester hydrolase
 F;108-222/Domain: glucose-6-phosphatase catalytic domain homology <GPH>

Query Match

Best Local Similarity 40.8%; Score 485; DB 1; Length 250;
 Matches 97; Conservative 29; Mismatches 76; Indels 0; Gaps 0;

Qy 23 EAINSLALPPPAVGSIAPLNDQAMYEQGRLLRTERGKLAEDANLSSGGVANAFAFGSA 82
 Db 31 EAVNSQFLPPPPGNDPAVYDEAYFGVAYKIGSPRMQQAEDADVENVNARLFSPV 90
 Qy 83 FGSPITEKDAAPALHKLITNMIEDAGLATRSKADHYMRIRPFAFYGVSTCTTEQDKLSK 142
 Db 91 VGAKINPKDPEPTNMMLKNLLTMGGYATASAKKTYMRTPVLFNHSITCRPEDENTLRK 150
 Qy 143 NGSPSGHTSIGMATLVLAELNIPORNEILKGYELGQSRVIGCYHMQSDVDAARVGS 202
 Db 151 NGSPSGHTSIGMATLVLAELNIPORNEILKGYELGQSRVIGCYHMQSDVDAARVGS 210

Qy 203 AVATLHTNPAFOQLQAKAE 224
 Db 211 VEFARLQITPAFOKSLAKVREE 232

RESULT 4

AF1025
 acid phosphatase (EC 3.1.3.2) - Salmonella enterica subsp. enterica serovar Typh (extra
 C;Species: Salmonella enterica subsp. enterica serovar Typh
 A;Note: this species has also been called Salmonella typhi
 C;Date: 09-Nov-2001 #sequence revision 09-Nov-2001 #text_change 25-Aug-2003
 A;Accession: AF1025
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
 th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Mole, S.; O'Garra, P.
 Nature 413, 848-852, 2001
 A;Author: Farry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skellon, J.; Stevens, K
 A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero
 A;Reference number: AB0502; MUID:21534947; PMID:11677608
 A;Accession: AF1025
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-250 <PAR>
 A;Cross-references: GB:AL513382; PID:CAD09303.1; PID:G16505305; GSPDB:GN00176
 C;Genetics:
 A;Gene: phoN
 C;Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic d
 C;Keywords: phosphoric monoester hydrolase

Query Match
 Best Local Similarity 40.1%; Score 477; DB 2; Length 250;
 Matches 95; Conservative 31; Mismatches 76; Indels 0; Gaps 0;

Qy 23 EAINSLALPPPAVGSIAPLNDQAMYEQGRLLRTERGKLAEDANLSSGGVANAFAFGSA 82
 Db 31 EAVNSQFLPPPPGNDPAVYDEAYFGVAYKIGSPRMQQAEDADVENVNARLFSPV 90
 Qy 83 FGSPITEKDAAPALHKLITNMIEDAGLATRSKADHYMRIRPFAFYGVSTCTTEQDKLSK 142
 Db 91 VGAKINPKDPEPTNMMLKNLLTMGGYATASAKKTYMRTPVLFNHSITCRPEDENTLRK 150
 Qy 143 NGSPSGHTSIGMATLVLAELNIPORNEILKGYELGQSRVIGCYHMQSDVDAARVGS 202
 Db 151 DGSYPGHTSIGMATLVLAELNIPORNEILKGYELGQSRVIGCYHMQSDVDAARVGS 210
 Qy 203 AVATLHTNPAFOQLQAKAE 224
 Db 211 VEFARLQITPAFOKSLAKVREE 232

RESULT 5

A32044
 acid phosphatase (EC 3.1.3.2) - Zymomonas mobilis
 C;Species: Zymomonas mobilis
 C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
 A;Accession: A32044
 R;Pond, J.L.; Eddy, C.K.; Mackenzie, K.F.; Conway, T.; Borecky, D.J.; Ingram, L.O.
 J. Bacteriol. 171, 767-774, 1989
 A;Title: Cloning, sequencing, and characterization of the principal acid phosphatase, th
 A;Reference number: A32044; MUID:89123152; PMID:2914872
 A;Accession: A32044
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-264 <PON>
 A;Cross-references: UNIPROT:P14924; GB:M24141; NID:G155613; PID:AAA27700.1; PID:G155614
 C;Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic do
 C;Keywords: phosphoric monoester hydrolase
 F;99-212/Domain: glucose-6-phosphatase catalytic domain homology <GPH>

Query Match
 Best Local Similarity 27.6%; Score 329; DB 1; Length 264;
 Matches 75; Conservative 37; Mismatches 97; Indels 4; Gaps 2;

.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183: 4823-4838, 2001
 A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1C
 A/Accession number: A96900; MUID:21359325; PMID:21359325
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-591 <KUR>
 A/Cross-references: UNIPROT:097124; GB:AE001437; PIDN:AAK78718.1; PID:G15023624; GSPDB:G
 A/Experimental source: Clostridium acetobutylicum ATCC824
 A/Genes: CAC0742

Query Match 13.2%; Score 157; DB 2; Length 591;
 Best Local Similarity 25.7%; Pred. No. 6.4e-06;
 Matches 71; Conservative 37; Mismatches 100; Indels 68; Gaps 13;

QY 1 LALVATGNDTTKPLLY-ALKNSAINTLALPP-PAVGSIA---FLNDQMYEQR 53
 DB 25 LARSVNGEITSHAAVGVFVDEMNNTNMSPSTNPAIGVLSGLKMKPGISYDNGI 84
 QY 54 LRNT-----ERKLAEDANTLS-----GGVANAFA---SGAFG 84
 DB 85 KLSNIDILNITQKVIQITVRRSTPOEHAVIDDRNONYSVLDELGYKDAFTKGAG-G 143
 QY 85 SPTE---KDAPALHKLIT-----NKIEDAGDL-----ATRSAXDHYM 119
 DB 144 TTIDVIRKD--AINVOYTDKNAEGWAEESSDLSGVVLTVDITNSAASITPAKYYK 201
 QY 120 RIRPAPYFV-STGNTEODKL---SKNGSPSGHTSIGMATAVLAETINPORONEILR 175
 DB 202 YPRFMRMDKVKVPLTVPEKSTNPSDDGPGPSHTNAATITDIALAVYPERVQEMLTR 261
 QY 176 GYEIGQSRVTCGYHWSQVDPAARVGSAAVATLHTN 211
 DB 262 ASELGNDRIVAGMHSPLDIVIGRYMATATAASALNN 297

RESULT 10
 AB3118
 serine proteinase Atu4566 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C/Species: Agrobacterium tumefaciens
 C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 C/Accession: AB3118
 R/Wood, D.W.; Secubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chan, Y.; Woo, I.
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.
 A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A/Reference number: AB2577; MUID:21608550; PMID:11743193
 A/Accession: AB3118
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-660 <KUR>
 A/Cross-references: UNIPROT:08U788; GB:AE008689; PIDN:AA45360.1; PID:G17743054; GSPDB:G
 A/Experimental source: strain C58 (Dupont)
 A/Genes: Atu4566
 A/Map position: linear chromosome

Query Match 11.8%; Score 141; DB 2; Length 660;
 Best Local Similarity 33.0%; Pred. No. 0.00019;
 Matches 29; Conservative 20; Mismatches 33; Indels 6; Gaps 1;

QY 141 SKNGSPSGHTSIGMATAVLAETINPORONEILKRGYELGQSRVTCGYHWSQVDPAARV 200
 DB 288 AKDGFSPSGHTNAYLAIAVAVPERFSELTLTAASELGSRIVAGMHSPLDIVIGRIT 347
 QY 201 GSAVATLHTNPAFOOQLQAKAEPAQH 228
 DB 348 ATMAAAMLODP-----KNAEYKKAH 369

RESULT 11
 E98169
 serine proteinase XF0267 [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
 C/Species: Agrobacterium tumefaciens
 C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
 C/Accession: E98169
 R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
 A.; Liu, F.; Kollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.
 Science 294, 2323-2328, 2001
 A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu
 A/Reference number: A97359; MUID:21608551; PMID:11743194
 A/Accession: E98169
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-660 <KUR>
 A/Cross-references: UNIPROT:08U788; GB:AE007870; PIDN:AAK88879.1; PID:G15158646; GSPDB:G
 A/Genes: AGR_L_612
 A/Map position: linear chromosome

Query Match 11.8%; Score 141; DB 2; Length 660;
 Best Local Similarity 33.0%; Pred. No. 0.00019;
 Matches 29; Conservative 20; Mismatches 33; Indels 6; Gaps 1;

QY 141 SKNGSPSGHTSIGMATAVLAETINPORONEILKRGYELGQSRVTCGYHWSQVDPAARV 200
 DB 288 AKDGFSPSGHTNAYLAIAVAVPERFSELTLTAASELGSRIVAGMHSPLDIVIGRIT 347
 QY 201 GSAVATLHTNPAFOOQLQAKAEPAQH 228
 DB 348 ATMAAAMLODP-----KNAEYKKAH 369

RESULT 12
 F75447
 vanadium chloroperoxidase-related protein - Deinococcus radiodurans (strain R1)
 C/Species: Deinococcus radiodurans
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C/Accession: F75447
 R/White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; F
 S.; Smith, H.O.; Venter, J.C.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
 Science 286, 1571-1577, 1999
 A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A/Reference number: A75250; MUID:20036896; PMID:10567266
 A/Accession: F75447
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-145 <WHI>
 A/Cross-references: UNIPROT:09RVL3; GB:AE001953; GB:AE000513; NID:G6458740; PIDN:AAF1058;
 A/Experimental source: strain R1
 A/Genes: DR1014
 A/Map position: 1

Query Match 8.8%; Score 105; DB 2; Length 145;
 Best Local Similarity 37.5%; Pred. No. 0.041;
 Matches 24; Conservative 9; Mismatches 31; Indels 0; Gaps 0;

QY 145 SYPSGHTSIGMATAVLAETINPORONEILKRGYELGQSRVTCGYHWSQVDPAARV 204
 DB 77 SYPSGHTVSGAAEVLAAQFFPLQARQLRRDADAFSRVVGIIHGVGVAGLVGQRY 136
 QY 205 VATL 208
 DB 137 ABAL 140

RESULT 13
 A87623
 PAP2 homolog protein [imported] - Caulobacter crescentus

C/Species: Caulobacter crescentus
 C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C/Accession: A87623
 R/Nieman, W.C.; Fieldlynn, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, U.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A/Title: Complete Genome Sequence of Caulobacter crescentus.
 A/Reference number: A87249; MUID:21173698; PMID:11259647
 A/Accession: A87623
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-259 <STO>
 A/Cross-references: UNIPROT:Q9A424; GB:AE005673; NID:g13424659; PIDN:AAK24981.1; GSPDB:C
 C/Genetics:
 A/Gene: CC3019
 C/Superfamily: bacitracin transport permease, glucose-6-phosphatase catalytic domain hom

Query Match 8.4%; Score 99.5; DB 2; Length 259;
 Best Local Similarity 28.0%; Pred. No. 0.27;
 Matches 47; Conservative 15; Mismatches 63; Indels 43; Gaps 5;

QY 70 LSSGVANAFSGAFSPITEKDALHK-LITNMIEDA----- 106
 DB 76 LRVGQPNALVGPFWLHVAADITAGVAVLTLLILAFALLGSLKRTAMLTALGAL 135
 QY 107 -GDATRSAXDHVIRPFAFYGVSTCMTTBDKLSKNGSPSGHTSIGMATAVL----- 161
 DB 136 SGVTVSQGLKAVFGERDEARIVE-----AVNASFSGHAMSAVVFLLGVLA 186

QY 162 AEINPQRNELLKRGY-----LGOSRVICGYHMQSDVDARVVGSA 203
 DB 187 ARFSRRRVKTLVSAAVVSLVGSARVYLGVMHVSVDVLAGWSVGA 234

RESULT 14
 D82070
 conserved hypothetical protein VC2488 [imported] - Vibrio cholerae (strain N16961 serog
 C/Species: Vibrio cholerae
 C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C/Accession: D82070
 R/Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F.L.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A/Reference number: A82035; MUID:20406833; PMID:10952301
 A/Accession: D82070
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-178 <HEI>
 A/Cross-references: UNIPROT:Q9K85; GB:AE004318; GB:AE003852; NID:g9657063; PIDN:AAF9563
 A/Experimental source: serogroup O1; strain N16961; biotype El Tor
 C/Genetics:
 A/Gene: VC2488
 A/Map position: 1
 C/Superfamily: bacitracin transport permease, glucose-6-phosphatase catalytic domain hom

Query Match 8.1%; Score 96; DB 2; Length 178;
 Best Local Similarity 31.0%; Pred. No. 0.34;
 Matches 27; Conservative 14; Mismatches 42; Indels 4; Gaps 1;

QY 115 KDHWRRIRPFAFYGVSTCMTTBDKLSKNGSPSGHTSIGMATAVLAEINPQRNELLK 174
 DB 81 KNSFQRRRPPQELASAVLTATYITPSDRY---SLPSGHTAAAFVMTLIGIYFHWYVALC 136

QY 175 RGEYIGOSRVICGYHMQSDVDARVVG 201
 DB 137 WAGLIGLARVLLGVHFLSDVITAGALLG 163

RESULT 15
 D87912

protein B0205.3 [imported] - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
 C/Accession: D87912
 R/Anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
 A/Reference number: A75000; MUID:99069613; PMID:9851916
 A/Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
 A/Accession: D87912
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-608 <STO>
 A/Cross-references: GB:chr_I; PIDN:ACI6991.1; PID:g3150473; GSPDB:GN00019; CESP:B0205.3
 C/Genetics:
 A/Gene: B0205.3
 A/Map position: 1

Query Match 7.8%; Score 93; DB 2; Length 608;
 Best Local Similarity 23.5%; Pred. No. 3.2;
 Matches 42; Conservative 19; Mismatches 78; Indels 40; Gaps 5;

QY 66 EDANLSSGVANAFSGAFSPITEKDALHKLITNMIEDAGDLATRSAXDHVIRPFA 125
 DB 456 EDGQAFGCGGNGMDNFMGMV-ENDPDLALALRVSMEEBRARQAAAAAN----- 505
 QY 126 FYGVSTCMTTBDKLSKNGSPSGHTSIG-----WATLVLAELINPQRNELLKRG 176
 DB 506 -GGADSGADAEVAAAAAVALPEEMDMGAMTEQOLEMALRLSMQENAPAEQPDV---- 559

QY 177 YELGOSRVICGYHMQSDVDARVVGSAVATLTHTNPAFOQ-----LQKAKAFQHQK 231
 DB 560 -----QHROMVDGAPAVGDNVLDLMMNPILLQIYVDLPAANAEKDDKEX 607

Search completed: March 2, 2005, 20:27:45
 Job time : 27.6667 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2005, 20:15:06 ; Search time 114.745 Seconds
(without alignments)
1030.696 Million cell updates/sec

Title: US-09-807-990A-124

Perfect score: 1190

Sequence: 1 LALVATGNDTTTKPDLYLK.....PAFQOOLQKAKAFQHQKK 231

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 10%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1190	100.0	249	Q9S1A6	Q9S1A6 escherichia
2	1095	92.0	248	Q9F1U0	Q9F1U0 enterobacte
3	1080	90.8	248	Q9F1U0	Q9F1U0 klebsiella
4	1065	88.5	248	Q9F1U0	Q9F1U0 klebsiella
5	1025	86.1	249	Q9S042	Q9S042 shigella fl
6	1022	85.9	249	Q9S099	Q9S099 shigella fl
7	986	82.9	248	PHON_PROST	P26975 providencia
8	969	81.4	249	PHOC_MORMO	P25581 morgarella
9	772	66.9	263	Q871B8	Q871B8 prevotella
10	582	48.9	246	Q9S035	Q9S035 shigella fl
11	577	48.5	246	Q9S099	Q9S099 shigella fl
12	576	48.4	246	Q9S1G8	Q9S1G8 escherichia
13	571	48.0	246	Q6XW11	Q6XW11 shigella fl
14	510.5	42.9	280	Q6AKP1	Q6AKP1 desulfotale
15	495.5	41.6	283	Q6AKN1	Q6AKN1 desulfotale
16	485	40.8	250	PHON_SALTY	P26976 salmoneila
17	478	40.2	250	Q8KRU6	Q8KRU6 salmoneila
18	477	40.1	250	PHON_SALTY	Q934J6 salmoneila
19	477	40.1	250	Q71EB8	Q71EB8 salmoneila
20	464	39.0	285	Q8BEI0	Q8BEI0 xanthomonas
21	433.5	36.4	280	Q8B342	Q8B342 xanthomonas
22	416.5	35.0	289	Q7TU08	Q7TU08 xanthomonas
23	329	27.6	264	PPA_ZYMMO	PPA_ZYMMO xanthomonas
24	274.5	23.1	258	Q9AB73	Q9AB73 caulobacter
25	220	18.5	231	Q9BHU7	Q9BHU7 rhizobium
26	189.5	15.9	2314	Q69822	Q69822 streptomyces
27	187	15.7	423	Q8ZLD5	Q8ZLD5 salmoneila
28	176.5	14.8	596	Q6SGX3	Q6SGX3 bacillus
29	172.5	14.5	241	Q916U4	Q916U4 pseudomonas
30	172	14.5	435	Q6D5H8	Q6D5H8 erwina car
31	157	13.2	591	Q97L24	Q97L24 clostridium

32	153.5	12.9	643	2	Q6FDK0	Q6FDK0 actinobact
33	149	12.5	986	2	Q87UJ2	Q87UJ2 pseudomonas
34	145.5	12.2	491	2	Q6A6B5	Q6A6B5 propionibac
35	144.5	12.1	128	2	Q7TUJ7	Q7TUJ7 prochloroco
36	144.5	12.1	657	2	Q87350	Q87350 ralsstonia s
37	143	12.0	622	2	Q8NR65	Q8NR65 cornebacte
38	142.5	12.0	115	2	Q6ZXV7	Q6ZXV7 pseudomonas
39	142.5	12.0	115	2	Q6ZXW1	Q6ZXW1 pseudomonas
40	141.5	11.9	115	2	Q6ZXW2	Q6ZXW2 pseudomonas
41	141	11.8	660	2	Q8U788	Q8U788 agrobacteri
42	139.5	11.7	115	2	Q6ZXV6	Q6ZXV6 pseudomonas
43	137.5	11.6	115	2	Q6ZXV8	Q6ZXV8 pseudomonas
44	129.5	10.9	513	2	Q8G856	Q8G856 bifidobacte
45	108	9.1	260	2	Q8E9E9	Q8E9E9 shewanella

ALIGNMENTS

RESULT 1

ID	Q9S1A6	PRELIMINARY:	PRT:	249 AA.
AC	Q9S1A6			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Acid phosphatase (EC 3.1.3.2).			
GN	Name=pho;			
OS	Escherichia blattae.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Escherichia.			
OX	NCBI_TaxID=563;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRATIN-UCM1650;			
RX	MEDLINE=20296667; PubMed=10835340; DOI=10.1093/emboj/19.11.2412;			
RA	Ishikawa K., Mihara Y., Gondoh K., Suzuki E., Asano Y.;			
RT	"X-ray structures of a novel acid phosphatase from Escherichia blattae			
RT	and its complex with the transition-state analog molybdate.";			
RL	EMBO J. 19:2412-2423 (2000).			
DR	EMBL; AB020481; BAA84942.1; .			
DR	PDB; 1D2T; X-ray; A/B/C=19-249.			
DR	PDB; 1E01; X-ray; A/B/C=19-249.			
DR	GO; GO:0030286; C:periplasmic space (sensu Gram-negative Bact. . . ; IEA.			
DR	GO; GO:0003959; F:acid phosphatase activity; IEA.			
DR	GO; GO:0016787; F:hydrolase activity; IEA.			
DR	InterPro; IPR011158; Acid_Phase_C1A1.			
DR	InterPro; IPR008934; ACPase VanPase.			
DR	InterPro; IPR001011; Bac_AcPaseAse.			
DR	InterPro; IPR000326; Peptidase_PA_PTP.			
DR	Pfam; PF01569; PAP2; 1.			
DR	PIRSF; PIRSF000897; Acid_Phase_C1A1; 1.			
DR	PRINTS; PRO0483; BACPHPTASE.			
DR	ProDom; PD009838; Bac_AcPaseAse; 1.			
DR	SMART; SM00014; acidPrc; 1.			
DR	PROSITE; PS01157; ACID_PHOSP_C1_A; 1.			
KW	Hydrolase.			
SC	SEQUENCE 249 AA; 26956 MW; 7ABAB6CB61FC0CA3 CRC64;			
Query Match	100.0%; Score 1190; DB 2; Length 249;			
Best local similarity	100.0%; Pred. No. 1.8e-99;			
Matches 231; Conservative	0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 LALVATGNDTTTKPDLYLKNSAINSTALLPPPAVGSIINFLNDQMYEGGRLLRNTER			60
Db	19 LALVATGNDTTTKPDLYLKNSAINSTALLPPPAVGSIINFLNDQMYEGGRLLRNTER			78
Qy	61 GKLAEDANLSSGGVANAFAFGSPITTEKDAFALHKLTLTMIDADGLATRSKADHYMR			120
Db	79 GKLAEDANLSSGGVANAFAFGSPITTEKDAFALHKLTLTMIDADGLATRSKADHYMR			138
Qy	121 IRPAFYGVSTCTTEDDKLSKNGSPSGHTSIGMATALLVLAIEINPORONEILKRGVELG			180

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Db 139 IRPFAFYGVSTCNTTEODKLSKNGSYPSGHTSIGMATLVLAELNFORONEILKRGYELG 198
Qy 181 OSRVICGYHMQSDVDAAARVGSAAVVALHTNPAFOOQLQKAKAFPAHQK 231
Db 199 OSRVICGYHMQSDVDAAARVGSAAVVALHTNPAFOOQLQKAKAFPAHQK 249

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RESULT 2

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Q9F1U1 PRELIMINARY; PRT; 248 AA.
ID O9F1U1
AC O9F1U1
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Acid phosphatase.
GN Name-pho;
OS Enterobacter aerogenes (aerobacter aerogenes).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Enterobacter.
OX NCBI_Taxid=548;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO12010;
RA Mihara Y., Utagawa T., Matsui H., Asano Y.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB044338; BAB18917.1; -.
DR HSSP; Q9S1A6; 1D2T.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR InterPro; IPR011158; Acid_Ptase_C1Aa.
DR InterPro; IPR008934; AcPase_VanFetase.
DR InterPro; IPR001011; Bac_AcPaseAa.
DR InterPro; IPR000326; Pesterase_PA_PTP.
DR Pfam; PF01569; PAP2; 1.
DR PIRSF; PIRSF000897; Acid_Ptase_C1Aa; 1.
DR PRINTS; PR00483; BACPHPTASE.
DR PRODOM; PD009838; Bac_AcPaseAa; 1.
DR SMART; SM00014; acidPc; 1.
DR PROSITE; PS01157; ACID_PHOSPH_CL_A; 1.
SQ SEQUENCE 248 AA; 26963 MW; 20EFA2C2E5EBE62D CRC64;

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Query Match 92.0%; Score 1095; DB 2; Length 248;
Best Local Similarity 92.1%; Pred. No. 7, 1e-91;
Matches 211; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

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```

Qy 2 ALVATGNDTTKPDLYLKNSAINSIALPPPAVGSIAFLNDQAMYEQRLIRTERG 61
Db 20 ALVPAAGNDATTKPDLYLKNAQAIDSLALPPPEVGSIAFLNDQAMYEKRLIRTERG 79
Qy 62 KLAEDANLSSGGVANAFAFGSPITTEKDA PALHKLITNMIEDAGDLATRSADHYMRI 121
Db 80 KLAEDANLSSGGVANAFAFGSPITTEKDA PALHKLITNMIEDAGDLATRSADHYMRI 139
Qy 122 RPFAYGVSTCNTTEODKLSKNGSYPSGHTSIGMATLVLAELNFORONEILKRGYELG 181
Db 140 RPFAYGVSTCNTTEODKLSKNGSYPSGHTSIGMATLVLAELNFORONEILKRGYELG 199
Qy 182 SRVICGYHMQSDVDAAARVGSAAVVALHTNPAFOOQLQKAKAFPAHQK 230
Db 200 SRVICGYHMQSDVDAAARVGSAAVVALHTNPAFOOQLQKAKAFPAHQK 248

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RESULT 3

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Q9F1U0 PRELIMINARY; PRT; 248 AA.
ID O9F1U0
AC O9F1U0
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Acid phosphatase.
GN Name-pho;
OS Klebsiella planticola (Raoultella planticola).

```

```

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Raoultella.
OX NCBI_Taxid=575;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO14939;
RA Mihara Y., Utagawa T., Matsui H., Asano Y.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB044345; BAB18918.1; -.
DR HSSP; Q9S1A6; 1D2T.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR InterPro; IPR011158; Acid_Ptase_C1Aa.
DR InterPro; IPR008934; AcPase_VanFetase.
DR InterPro; IPR001011; Bac_AcPaseAa.
DR InterPro; IPR000326; Pesterase_PA_PTP.
DR Pfam; PF01569; PAP2; 1.
DR PIRSF; PIRSF000897; Acid_Ptase_C1Aa; 1.
DR PRINTS; PR00483; BACPHPTASE.
DR PRODOM; PD009838; Bac_AcPaseAa; 1.
DR SMART; SM00014; acidPc; 1.
DR PROSITE; PS01157; ACID_PHOSPH_CL_A; 1.
SQ SEQUENCE 248 AA; 26745 MW; 68F65CA2448BB3EF CRC64;

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Query Match 90.8%; Score 1080; DB 2; Length 248;
Best Local Similarity 90.8%; Pred. No. 1, 6e-89;
Matches 208; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

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```

Qy 2 ALVATGNDTTKPDLYLKNSAINSIALPPPAVGSIAFLNDQAMYEQRLIRTERG 61
Db 20 ALVPAAGNDATTKPDLYLKNAQAIDSLALPPPEVGSIAFLNDQAMYEKRLIRTERG 79
Qy 62 KLAEDANLSSGGVANAFAFGSPITTEKDA PALHKLITNMIEDAGDLATRSADHYMRI 121
Db 80 KLAEDANLSSGGVANAFAFGSPITTEKDA PALHKLITNMIEDAGDLATRSADHYMRI 139
Qy 122 RPFAYGVSTCNTTEODKLSKNGSYPSGHTSIGMATLVLAELNFORONEILKRGYELG 181
Db 140 RPFAYGVSTCNTTEODKLSKNGSYPSGHTSIGMATLVLAELNFORONEILKRGYELG 199
Qy 182 SRVICGYHMQSDVDAAARVGSAAVVALHTNPAFOOQLQKAKAFPAHQK 230
Db 200 SRVICGYHMQSDVDAAARVGSAAVVALHTNPAFOOQLQKAKAFPAHQK 248

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RESULT 4

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Q9RLW6 PRELIMINARY; PRT; 248 AA.
ID Q9RLW6
AC Q9RLW6
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Phoc protein precursor (BC 3.1.3.2).
GN Name-phoc;
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_Taxid=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCUG 225;
RA Pasarelliello C., Berlucchi F., Selan L., Thaller M.C., Rossolini G.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ250377; CAB59725.1; -.
DR HSSP; Q9S1A6; 1D2T.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0003993; F:hydrolyase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR011158; Acid_Ptase_C1Aa.
DR InterPro; IPR008934; AcPase_VanFetase.
DR InterPro; IPR001011; Bac_AcPaseAa.
DR InterPro; IPR000326; Pesterase_PA_PTP.
DR Pfam; PF01569; PAP2; 1.

```

DR PIRSF; PIRSF000897; Acid Phase_ClaA; 1.
 DR PRINTS; PR00483; BACPHPTASE. 1.
 DR PRODOM; PD009838; Bac_AcPaseA. 1.
 DR SMART; SM00014; acidPfc. 1.
 DR PROSITE; PS01157; ACID_PHOSP_CLA_A; 1.
 KW Hydrolyase; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 248 Phoc.
 SQ SEQUENCE 248 AA; 27110 MW; ED6E9D8663636B0D CRC64;

Query Match 89.5%; Score 1065; DB 2; Length 248;
 Best Local Similarity 89.5%; Pred. No. 3.7e-88;
 Matches 205; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 2 ALVAGNDTTTTPDLYLKNSEAINSLALPPPPAVGSAFLNDQAMYEQGLLNTNRG 61
 DB 20 ALVPGNDVTTKPDLYLTNNAIDSLALPPPPAVGSAFLNDQAMYEQGLLNTNRG 79
 QY 62 KLAEDANLSSGGVANAFAFGSPITEKDALPKLITNMIEDAGDLATRSADHYMRI 121
 DB 80 KLAEDANLSSGGVANAFAFGSPITEKDALPKLITNMIEDAGDLATRSADHYMRI 139
 QY 122 RPAFYGVSTCNTTEQDILKNGSYPSGHTSIGMATLVLAIEINPQRONEILKRGYELGQ 181
 DB 140 RPAFYGVSTCNTTEQDILKNGSYPSGHTSIGMATLVLAIEINPQRONEILKRGYELG 199
 QY 182 SRVCGYMWQSDVDAARVGSAVVAATLTNPAFOQOLQKAKAFPAHQK 230
 DB 200 SRVCGYMWQSDVDAARVGSAVVAATLTNPAFOQOLQKAKAFPAHQK 248

RESULT 5

OS0542 PRELIMINARY; PRT; 249 AA.

AC OS0542;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Nonspecific phosphatase.
 GN Name=phon;
 OS Shigella flexneri.
 OG Plasmid pMYSH6000.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Shigella.
 OX NCBI_TaxID=623;
 RN RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=SH6000;
 RX MEDLINE=96345620; PubMed=8755883;
 RA Uchiya K., Tobuaji M., Nikai T., Sugihara H., Sasakawa C.;
 RT "Identification and characterization of phon-Sf, a gene on the large
 RT plasmid of Shigella flexneri 2a encoding a nonspecific phosphatase.";
 RL J. Bacteriol. 178:4548-4554(1996).
 RN RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=SH6000;
 RA Uchiya K.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; D82966; BAA11655.1; -.
 DR HSSP; Q9S1A6; 1D2T.
 DR GO; GO:0003028; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
 DR GO; GO:0003993; F:acid phosphatase activity; IEA.
 DR InterPro; IPR01158; Acid_Ptase_ClaA.
 DR InterPro; IPR008934; AcPase_VanPase.
 DR InterPro; IPR01011; Bac_AcPaseA.
 DR Pfam; PF01569; PAP2; 1.
 DR PIRSF; PIRSF000897; Acid Phase_ClaA; 1.
 DR PRINTS; PR00483; BACPHPTASE.
 DR PRODOM; PD009838; Bac_AcPaseA. 1.
 DR SMART; SM00014; acidPfc. 1.
 DR PROSITE; PS01157; ACID_PHOSP_CLA_A; 1.
 KW Plasmid.

SQ SEQUENCE 249 AA; 27177 MW; 58F34CEB034EB070 CRC64;
 Query Match: 86.1%; Score 1025; DB 2; Length 249;
 Best Local Similarity 84.8%; Pred. No. 1.6e-84;
 Matches 195; Conservative 14; Mismatches 21; Indels 0; Gaps 0;

QY 2 ALVAGNDTTTTPDLYLKNSEAINSLALPPPPAVGSAFLNDQAMYEQGLLNTNRG 61
 DB 20 ASIPGNDVTTKPDLYLTNNAIDSLALPPPPGIGSAFLNDQAMYEKRLNTNRG 79
 QY 62 KLAEDANLSSGGVANAFAFGSPITEKDALPKLITNMIEDAGDLATRSADHYMRI 121
 DB 80 KLAEDANLSSGGVANAFAFGSPITEKDALPKLITNMIEDAGDLATRSADHYMRI 139
 QY 122 RPAFYGVSTCNTTEQDILKNGSYPSGHTSIGMATLVLAIEINPQRONEILKRGYELGQ 181
 DB 140 RPAFYGVSTCNTTEQDILKNGSYPSGHTSIGMATLVLAIEINPARDTLLKRGYELG 199
 QY 182 SRVCGYMWQSDVDAARVGSAVVAATLTNPAFOQOLQKAKAFPAHQK 231
 DB 200 SRVCGYMWQSDVDAARVGSAVVAATLTNPAFOQOLQKAKAFPAHQK 249

RESULT 6

Q99099 PRELIMINARY; PRT; 249 AA.

AC Q99099; Q7BCK1;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Phon1, periplasmic non specific acid ohosphatase (Phosphatase
 DE precursor).
 GN Name=phon1; Synonyms=phon-Sf;
 OS Shigella flexneri.
 OG Plasmid virulence plasmid pWR501, and Plasmid pC9301.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Shigella.
 OX NCBI_TaxID=623;
 RN RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=M90T;
 RX MEDLINE=20566792; PubMed=11115111;
 RA Buchrieser C., Glaeser P., Rusnok C., Nedjari H., d'Hauteville H.,
 RA Kunst F., Sansonetti P., Parrot C.;
 RT "The virulence plasmid pWR100 and the repertoire of proteins secreted
 RT by the type III secretion apparatus of Shigella flexneri.";
 RL Mol. Microbiol. 38:760-771(2000).
 RN RN
 RP SEQUENCE FROM N.A.
 RC PLASMID=virulence plasmid pWR501;
 RX MEDLINE=21189246; PubMed=11292750;
 RX DOI=10.1128/JAI.69.5.3471-3285.2001;
 RA Venkatesan M.M., Goldberg M.B., Rose D.J., Grotbeck E.J., Burland V.,
 RA Blattner F.R.;
 RT "Complete DNA sequence and analysis of the large virulence plasmid of
 RT Shigella flexneri.";
 RL Infect. Immun. 69:3271-3285(2001).
 RN RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=301 / Serotype 2a; PLASMID=PC9301;
 RX MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
 RA Jin Q., Yan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
 RA Yang D., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
 RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
 RA Chang H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
 RA Yu J.;
 RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
 RT through comparison with genomes of Escherichia coli K12 and O157.";
 RL Nucleic Acids Res. 30:4432-4441(2002).
 DR EMBL; AL381753; CAC05839.1; -.
 DR EMBL; AF348706; AAK18512.1; -.
 DR EMBL; AF386526; AAL72311.1; -.
 DR HSSP; Q9S1A6; 1D2T.

DR GO: GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
 DR GO: GO:0003993; F:acid phosphatase activity; IEA.
 DR InterPro: IPR01158; Acid_Phase_C1aA.
 DR InterPro: IPR008934; AcPase_VanPerase.
 DR InterPro: IPR001011; Bac_AcPaseA.
 DR InterPro: IPR000326; Pesterase_PA_PTP.
 DR Pfam: PF01569; PAP2_1.
 DR PIRSF: PIRSF000897; Acid_Phase_C1aA_1.
 DR PRINTS: PR00483; BACPHPTASE.
 DR ProDom: PD009838; Bac_AcPaseA.
 DR SMART: SM00014; acidppc; 1.
 DR PROSITE: PS01157; ACID_PHOSP_C1_A; 1.
 DR Complete proteome; Plasmid.
 KW SEQUENCE 249 AA; 27211 MW; 9051C6C1CCE21ABA CRC64;

Query Match 85.9%; Score 1022; DB 2; Length 249;
 Best Local Similarity 86.2%; Pred. No. 2.9e-84;
 Matches 194; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

QY 7 GNDTTKPDLYLKNSSEAINSLALPPPAVGSIATLNDQMYEQGRLLNTERG 66
 DB 25 GNDVTKPDLYLKNSQADISLALPPPEVGSILFLNDQMYEKGRLLNTERG 79
 QY 67 DANLSSGGVANAFAFGSPITEKDAPELHKLITNMTEDAGDLATRSKDHVRIPEAF 126
 DB 85 DANLSSGGVANAFAFGSPITAKDSPELHKLITNMTEDAGDLATRSKDHVRIPEAF 144
 QY 127 YGVSTCNTTEODKLSKNSYSPGHTSIGMATATLAEINPORONEILKRGYEIGQ 181
 DB 145 YGVSTCNTTEODKLSKNSYSPGHTSIGMATATLAEINPORONEILKRGYEIGQ 199
 QY 187 GYHWSQDVDAARIVASAVATLTNPAFPOOLOKAKAFQHOXK 230
 DB 205 GYHWSQDVDAARIVASAVATLTNPAFPOOLOKAKAFQHOXK 248

RESULT 7

PHON_PROST STANDARD; PRT; 248 AA.
 AC P26975;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DE Nonspecific acid phosphatase precursor (EC 3.1.3.2) (NSAP).
 GN Name-phoc;
 OS Providencia stuartii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Providencia.
 OX NCBI_TaxID=588;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PV81;
 RA Riccio M.L., Lombardi G., Chiesurin A., Satta G.;
 RL Submitted (FEB-1992) to the EMBL/Genbank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: A phosphate monoester + H(2)O = an alcohol +
 CC phosphate.
 CC -1- SUBCELLULAR LOCATION: Periplasmic.
 CC -1- SIMILARITY: Belongs to the class A bacterial acid phosphatase
 CC family.
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 CC or send an email to license@ebi.ac.uk).
 CC EMBL: X64820; CAA46032.1; -.
 DR PIR: S19888; PAOFC3.
 DR HSSP: Q9S1A6; 1D2T.
 DR InterPro: IPR01158; Acid_Phase_C1aA.
 DR InterPro: IPR008934; AcPase_VanPerase.

DR InterPro: IPR001011; Bac_AcPaseA.
 DR InterPro: IPR000326; Pesterase_PA_PTP.
 DR Pfam: PF01569; PAP2_1.
 DR PIRSF: PIRSF000897; Acid_Phase_C1aA_1.
 DR PRINTS: PR00483; BACPHPTASE.
 DR ProDom: PD009838; Bac_AcPaseA.
 DR SMART: SM00014; acidppc; 1.
 DR PROSITE: PS01157; ACID_PHOSP_C1_A; 1.
 DR HydroLase; Periplasmic Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 248
 FT POTENTIAL 1
 KW SEQUENCE 248 AA; 27043 MW; 2122A4B95E767CB2 CRC64;

Query Match 82.9%; Score 986; DB 1; Length 248;
 Best Local Similarity 81.2%; Pred. No. 5.3e-81;
 Matches 186; Conservative 24; Mismatches 19; Indels 0; Gaps 0;

QY 2 ALVATGNTTKPDLVYKNSSEAINSLALPPPAVGSIATLNDQMYEQGRLLNTERG 61
 DB 20 ALVATGNTTKPDLVYKNSQADISLALPPPEVGSILFLNDQMYEKGRLLNTERG 79
 QY 62 KLAABDANLSSGGVANAFAFGSPITEKDAPELHKLITNMTEDAGDLATRSKDHVRI 121
 DB 80 KLAABDANLSSGGVANAFAFGSPITEKDAPELHKLITNMTEDAGDLATRSKDHVRI 139
 QY 122 RPPAFYGVSTCNTTEODKLSKNSYSPGHTSIGMATATLAEINPORONEILKRGYEIGQ 181
 DB 140 RPPAFYGVSTCNTTEODKLSKNSYSPGHTSIGMATATLAEINPORONEILKRGYEIGQ 199
 QY 182 SRVICYHWSQDVDAARIVASAVATLTNPAFPOOLOKAKAFQHOXK 230
 DB 200 SRVICYHWSQDVDAARIVASAVATLTNPAFPOOLOKAKAFQHOXK 248

RESULT 8

PHOC_MORMO STANDARD; PRT; 249 AA.
 AC P28581;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DE Major phosphate-irrepressible acid phosphatase precursor (EC 3.1.3.2)
 GN (HPAP).
 OS Moraxella morganii (Proteus morganii).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Moraxella.
 OX NCBI_TaxID=582;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 21-40.
 RC STRAIN=RS12;
 RA MEDLINE=94362901; PubMed=8081499;
 RL Thaller M.C., Berluti F., Schippa S., Lombardi G., Rosolini G.M.;
 CC "Characterization and sequence of Phoc, the principal phosphate-
 CC irrepressible acid phosphatase of Moraxella morganii";
 CC Microbiology 140:1341-1350 (1994).
 CC [2]
 CC SEQUENCE FROM N.A.
 RC STRAIN=NCIMB 10466;
 RX MEDLINE=20336426; PubMed=10877772;
 RX DOI=10.1128/AEM.66.7.2811-2816.2000;
 RA Mihara Y., Udagawa T., Yamada H., Asano Y.;
 RL "Phosphorylation of nucleosides by the mutated acid phosphatase from
 RL Moraxella morganii";
 CC Appl. Environ. Microbiol. 66:2811-2816 (2000).
 CC -1- CATALYTIC ACTIVITY: A phosphate monoester + H(2)O = an alcohol +
 CC phosphate.
 CC -1- SUBUNIT: Homotrimer.
 CC -1- SUBCELLULAR LOCATION: Periplasmic.
 CC -1- MISCELLANEOUS: Has a pH optimum around 6.
 CC -1- SIMILARITY: Belongs to the class A bacterial acid phosphatase
 CC family.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; X64444; CAA45774.1; -
DR EMBL; AB035805; BAA96744.1; -
DR PIR; S19187; S19187.
DR HSSP; Q9S1A6; 1D2T.
DR InterPro; IPR011158; Acid Phase ClsA.
DR InterPro; IPR008934; AcPase VanPase.
DR InterPro; IPR001011; Bac AcPasease.
DR InterPro; IPR000326; Peptidase_PA_PTP.
DR Pfam; PF01569; PAP2; 1.
DR PIRSF; PIRSF00897; Acid Phase ClsA; 1.
DR PRINTS; PR00483; BACPHPTASE.
DR ProDom; PD009838; Bac AcPasease; 1.
DR SMART; SM00014; acidPfc; 1.
DR PROSITE; PS01157; ACID_PHOSP_CL_A; 1.
KW Direct protein sequencing; Hydrolase; Periplasmic; Signal.
FT SIGNAL 1 20
FT CHAIN 21 249 Major phosphate-irrepressible acid
FT phosphate.
SQ SEQUENCE 249 AA; 26998 MW; C43F3698052B6A5C CRC64;
Query Match 81.4%; Score 969; DB 1; Length 249;
Best Local Similarity 79.2%; Pred. No. 1.9e-79;
Matches 183; Conservative 20; Mismatches 28; Indels 0; Gaps 0;

QY 1 LALVATGDDTTKPLLYLYKNSAINSLLALPPPPAVGSIAPLNDQMYEQRLNTER 60
DB 19 LALPAGADATTKPLLYLYKNEAIDSLKLPPPEVGSIOPLNDQMYEQRLNTER 78
QY 61 GKLAEDNANLSSGVANAFSGAFSPITEKDALHKLNTNMIEDAGDLATRSADHYMR 120
DB 79 GKQADADDLAAGVATAFSGAFSPITEKDSPELYKLTNMIEDAGDLATSAEHYMR 138
QY 121 IRPFAFVSTCNTTETODKLSKNGSPSGHTSIGNATLVLAELNPPORNEILKGYELG 180
DB 139 IRPFAFVSTCNTTETODKLSKNGSPSGHTSIGNATLVLAELNPPANDAILERGYQLG 198
QY 181 QSRVTCGYHMOVDVAAVAVATLHTNPAFOOOLAKAKAFPHOKK 231
DB 199 QSRVTCGYHMOVDVAAVAVATLHTNPAFOOOLAKAKAFPHOKK 249

RESULT 9
ID 087188 PRELIMINARY; PRT; 263 AA.
AC 087188;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Acid phosphatase (PACP) precursor.
GN Name=PnOC;
OS Prevotella intermedia.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Prevotellaceae; Prevotella.
OX NCBI_TaxID=26131;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 25611;
RX MEDLINE=20026825; PubMed=10559178;
RA Chen X., Ansat T., Awano S., Iida T., Barik S., Takehara T.;
RT "Isolation, cloning, and expression of an acid phosphatase containing
RT phosphotyrosyl phosphatase activity from Prevotella intermedia.";
RL J. Bacteriol. 181:7107-7114(1999).
DR EMBL; AB017537; BAA33148.1; -
DR HSSP; Q9S1A6; 1D2T.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . . ; IEA.

DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR InterPro; IPR011158; Acid Phase ClsA.
DR InterPro; IPR008934; AcPase VanPase.
DR InterPro; IPR001011; Bac AcPasease.
DR InterPro; IPR000326; Peptidase_PA_PTP.
DR Pfam; PF01569; PAP2; 1.
DR PIRSF; PIRSF00897; Acid Phase ClsA; 1.
DR PRINTS; PR00483; BACPHPTASE.
DR ProDom; PD009838; Bac AcPasease; 1.
DR SMART; SM00014; acidPfc; 1.
DR PROSITE; PS01157; ACID_PHOSP_CL_A; 1.
KW Signal.
FT SIGNAL 1 20 Potential.
SQ SEQUENCE 263 AA; 29201 MW; 6AD1C4A6470BF313 CRC64;
Query Match 64.9%; Score 772; DB 2; Length 263;
Best Local Similarity 65.9%; Pred. No. 1.4e-61;
Matches 147; Conservative 28; Mismatches 48; Indels 0; Gaps 0;

QY 9 DTTKPDLYLYKNSAINSLLALPPPPAVGSIAPLNDQMYEQRLNTERGKLAADA 68
DB 29 DARTPDIYLYQDGGQTSLELPPPPGSIQPLYDAQYQMGQMQRTRGDQAVADA 88
QY 69 NLSGVANAFSGAFSPITEKDALHKLNTNMIEDAGDLATRSADHYMRIRPFAFG 128
DB 89 RVGGDGVNAPSEAFSGIKSKETPEIKYLVNMRDAGDLATRSADHYMRVRFAPYN 148
QY 129 VSTCNTTETODKLSKNGSPSGHTSIGNATLVLAELNPPORNEILKGYELGQSRVTCGY 188
DB 149 EMTCTNPEEQOELSTNGSPSGHTSIGNATLVLAELNPPORNEILERGYQMGQSRVTCGY 208
QY 189 HMOSVDVAAVAVAVATLHTNPAFOOOLAKAKAFPHOKK 231
DB 209 HMOSVDVAAVAVAVATLHTNPAFOOOLAKAKAFPHOKK 251

RESULT 10
ID 0990G5 PRELIMINARY; PRT; 246 AA.
AC 0990G5;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE PnO2 (Apy), periplasmic phosphatase, apyrase, ATP diphosphohydrolase
DE (Apyrase)
GN Name=pnO2 (apy); Synonym=S0004;
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M90T;
RX MEDLINE=20566792; PubMed=1115111;
RX Buchrieser C., Glaser P., Ruenick C., Nedjari H., d'Haevillie H.,
RA Kunst F., Sansonetti P., Parrot C.,
RT "The virulence plasmid pWR100 and the repertoire of proteins secreted
RT by the type III secretion apparatus of Shigella flexneri.";
RL Mol. Microbiol. 38:760-771(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC PLASMID=virulence plasmid pWR501;
RX MEDLINE=21189246; PubMed=11292750;
RX DOI=10.1128/JAI.69.5.3271-3285.2001;
RA Verketesan M.M., Goldberg M.B., Rose D.J., Grotbeck B.J., Burland V.,
RA Blatter F.R.;
RT "Complete DNA sequence and analysis of the large virulence plasmid of
RT Shigella flexneri.";
RL Infect. Immun. 69:3271-3285(2001).
DR EMBL; AL391753; CAC05771.1; -
DR HSSP; AF348706; AAK18315.1; -
DR HSSP; Q9S1A6; 1I18.

DR GO: 00030288; C:peptidase space (sensu Gram-negative Bact. . .; IEA.
DR GO: 00033993; F:acid phosphatase activity; IEA.
DR GO: 0016787; F:hydrolase activity; IEA.
DR InterPro: IPR011158; Acid_Peasase_C1A8.
DR InterPro: IPR008934; AcPase_VanPase.
DR InterPro: IPR010111; Bac_AcPaseA.
DR InterPro: IPR003326; Pesterase_PA_PTP.
DR Pfam: PFO1569; PAP2; 1.
DR PIRSF: PIRSF000897; Acid_Peasase_C1A8; 1.
DR PRINTS: PRO0483; BACPMPHASE.
DR Prodom: PD009838; BacAcPaseA; 1.
DR SMART: SM00014; acidppc; 1.
KE Hydrolase; Peamid.
SQ SEQUENCE 246 AA; 27559 MW; 48D76BD8CC7885E5 CRC64;

Query Match	48.9%	Score 582;	DB 2;	Length 246;
Best Local Similarity	51.9%;	Pred. No. 2.1e-44;		
Matches 109;	Conservative 43;	Mismatches 56;	Indels 2;	Gaps 1

OY 18 YLKNSEATNSLLALPPPAVGSIAEFLNDQAMYEQGILLRTERGKLAEDANTSSGGVAN 77
 : | : : : ||| | | : | | : | | | | : : | : | : | : | :
Dd 29 FLTQOTSPPSLSTILPPPRAEDSVFVLADKAHYEFGRSLRANRVLASADAYENFGI-- 86

QY 78 AEGGAFGEITEKDA PALHKLITNNIEDAGDLATRS AKOHMYRIRPFAYGVSTCNTTEQ 137
||| : : : ||| : : : | : : : | : : : | : : :
Db 87 AEFDAYGMDISRENTPILYQLTVOLODSHDVAVENAKERYKRVPFVIYKDATCPBDKO 146

QY 138 DKLSKNGSYPSGHTSIGWATALVIAEINPQRONEILKRGEYGOSRVICGYHWQSDVDA 197
::: ||||| | | : ||||| : ||: ||||| : ||||| ||||| :
Db 147 EKVAITGSYPGGHASFQWAVALLAEINPQKAELIRRGVEFGESRIVCGAHMQSDVEAG 206

QY 198 RVVGSVVATLHTNPAPFOQLQKAKAEPAQ 227
|::|:| | | | : | : | | | :
Db 207 RLMGASVAVLHNTPEFTKSLSEAKKEFEE 236

RESULT 11
Q59909
ID Q59909
PRELIMINARY;
PRT; 246 AA.

DE	ATP diphosphohydrolyase, apyrase precursor (EC 3.6.1.5) (Amurao)
DT	25-OCT-2004 (Tremblrel). 28, Last annotation update)
DT	01-NOV-1996 (Tremblrel). 01, last sequence update)
DT	01-NOV-1996 (Tremblrel). 01, Created)

OS Shigella flexneri.
OG plasmid pCP301.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

```

OX  NCBI_TaxId=623;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=2a;

```

Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
[2]

STRAIN=2a;
ROY R.;
Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
[1]

STRAIN=301 / Serotype 2a; PLASMID=pcp301;
MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Ju W., Wang T., Liu H.

Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S., Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y., Yu J.;

through comparison with genomes of *Escherichia coli* K12 and O157." ;
Nucleic Acids Res. 30:4432-4441(2002).

DR EMBL; U04559; AAA21206.1; -.
DR EMBL; AF368526; AAL72358.1; -.
DR HSSP; Q9SL46; 11W8.
DR GO; GO:0030289; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR GO; GO:0004050; F:phosphatase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPRO1158; Acid phase ClsA.
DR InterPro; IPRO0934; Acetate VanErase.
DR InterPro; IPRO01011; Bac_AcGataseH.
DR InterPro; IPRO00326; pesterase_PA_PTP.
DR Pfam; PF01569; PAP2; 1.
DR PIRSF; PIRSF00897; Acid phase ClsA; 1.
DR PRINTS; PRO0483; BACPHPTASE.
DR ProDom; PD009839; Bac AcPataaseA; 1.
DR SMART; SM00014; acidPPc; 1.
KW Complete proteome; Hydrolase; Signal.
FT SIGNAL 1 23 Potential.
SQ SEQUENCE 246 AA; 27573 MW; B81737D9E6143912 CRC64;

Query Match	48.5%	Score 577	DB 2	Length 246
Best Local Similarity	51.4%	Pred. No. 6e-44		
Matches 108: Conservative	43	Mismatches	57	Indels 2
				Gaps 1

QY 18 YLKNSEAINSLALLPPPPVAGSIAFLINDQAMTEQGRLLIRNTERKGLAEDANILSSGGVAN 77
Db 29 FLTQOTSDSLSLTPPPPAENSVVFQADKAHTEFGRSIRJRDANRVRRLASEDAYENFCL-- 86

QY 78 A E S G A F G P I T E D K A P A L H K L T N M I E A G D I A T R S K D H V R I R P E A F Y G U S T C N T E Q 137
||| : : : : : ||| : : : : : ||| : : : : :
Db 87 A F S D A Y G M D I S B E N T F L I Y O L L I Q V L D S H D V A V R N A K E Y I R G R V R P E V I Y K D A T C T E D K D 146

147 EKAAITSSYPSGHASFGWAVAAIIILAEINPORKAEILRRGYEGESRYICGAHWQSDVEAG 206

Db 207 RLMGASVVAVLHNTPEFTKSLSEAKKEFEE 236

RESULT 12
 Q93IG8
 ID Q93IG8
 AC Q93IG8;
 PRELIMINARY;
 PRT; 246 AA.

DT	01-DEC-2001	(TEMBLrel. 19, last sequence update)
DT	01-OCT-2003	(TEMBLrel. 25, last annotation update)
DE	Apyrase (EC 3.6.1.5).	
DN	MSB000000000	

OS *Escherichia coli*.
OS Plasmid pHN280.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia

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RN      _ _ _ _ _
RP      SEQUENCE FROM N.A.
RC      STRAIN=HN280;
RY      _ _ _ _ _

```

RA Rastapadri D., Casalino M., Petrucci A., Presutti C., Zagaglia C.,
 RA Santucci F., Colonna B., Nicoletti M.,
 RT Enteroinvasive Escherichia coli virulence-plasmid-carrying apyrase
 (avp) and osmB genes are organized as a bifunctional operon

Microbiol. Cell. Expr. 148:2519-2529 (2002).
 DR EMBL: AJ315184; CAB67470.1; -.
 HSSP: Q951A6; I1W6.

DR GO: 0003993; F:acid phosphatase activity; IEA.
DR GO: 0004050; F:apsyrase activity; IEA.
DR GO: 0016787; F:hydrolase activity; IEA.
DR Inferro: tp00011 IEA:acid p-actv; IEA.

DR. JULECIO, LEK08334; ACRISE_VANPERASE.

DB 205 IVCNNAHQSDVMMGRINGCAVAVARLHADPAFLAEIEVAKALKAPRTK 252

RESULT 15

06AKN1 PRELIMINARY; PRT; 283 AA.
 AC 06AKN1, 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Probable acid phosphatase.
 GN OrderedLocustNames=Dp2385.
 OS Desulfotalea psychrophila.
 CC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacteriales;
 CC Desulfobulbaceae; Desulfotalea.
 OX NCBI_TaxID=84980;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LSY54 / DSM 12343;
 RX PubMed=15305914;
 RA Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M.,
 RA Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,
 RA Teeling H., Leuschner W.D., Glockner F.-O., Lupas A.N., Amann R.,
 RA Klenk H.-P.;
 RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
 from permanently cold Arctic sediments.";
 RL Environ. Microbiol. 6:887-902 (2004).
 DR EMBL; CR52870; CAG37094.1; -
 DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
 DR GO; GO:0003993; F:acid phosphatase activity; IEA.
 DR InterPro; IPR011158; F:acid phosphatase activity; IEA.
 DR InterPro; IPR008934; AcPase_VanFerae.
 DR InterPro; IPR001011; Bac_AcPaseA.
 DR InterPro; IPR000326; Pesterase_PA_PTP.
 DR Pfam; PF01569; PAP2; 1.
 DR PIRSF; PIRSF000897; Acid_Pase_C16a; 1.
 DR PRINTS; PR00483; BACPMPHASE.
 DR PRODOM; PD009838; BACPMPHASE; 1.
 DR SMART; SM00014; acidPfc; 1.
 KW Complete proteome.
 SQ SEQUENCE 283 AA; 30483 MW; 86DD9AEED704D632 CRC64;

Query Match 41.6%; Score 495.5; DB 2; Length 283;
 Best Local Similarity 48.8%; Pred. No. 1,7e-36;
 Matches 101; Conservative 30; Mismatches 75; Indels 1; Gaps 1;
 QY 18 YLKNSEAINSLALLPPPPVGSIAFLNDQAMTEQGRLLNTERGKLAEDANLSSGGVAN 77
 DB 43 YLPVDMLEPNSLTLIPPPAEGSTAFALDREVNRQSHALQGTARWNLAKRDARLKFPQAAE 102
 QY 78 AFSGAFGSPITEKDPALHKLITNMIEDAGDLATRSADKHMRIRPPAFYGVSTCNTTEQ 137
 DB 103 TFSICALGPISEAFERPHLYMLRLRTIADA-ILSTYKANQHYRRTRPPFLNGEPTCTPTKE 161
 QY 138 DKLKNGSYPSGHSISGNATLVLAELNPORENLKRGVELGOSRVICGYHMQSDVDA 197
 DB 162 AHMKSSGSPFSGHTAIGWAMALLIVEVAPEQTDAILANGWAFGOSRIICNVHMQSDVLMG 221
 QY 198 RVGSAVAVATLHTNPAFQOOLOKAAE 224
 DB 222 QVMGAAAVAKLHSDPAFLAEIEAAAE 248

Search completed: March 2, 2005, 20:26:48
 Job time : 117.745 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 2, 2005, 20:12:01 ; Search time 116.732 Seconds
(without alignments)
755.417 Million cell updates/sec

Title: US-09-807-990A-125

Perfect score: 1173
Sequence: 1 LVPAGNDATTKEDLYLKNA.....NPAFOQLQKAKDEPAKTQK 228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq.16dec04:*
1: geneeqp1980s:*
2: geneeqp1990s:*
3: geneeqp2000s:*
4: geneeqp2001s:*
5: geneeqp2002s:*
6: geneeqp2003as:*
7: geneeqp2003bs:*
8: geneeqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1173	100.0	248	AAW06458	AAW06458 Enterobac
2	1173	100.0	248	AAW71031	AAW71031 Acid phos
3	1139	97.1	253	ABO61416	ABO61416 Klebsiell
4	1136	96.8	248	AAW06459	AAW06459 Klebsiell
5	1136	96.8	248	AAW71032	AAW71032 Acid phos
6	1127	96.1	248	AAW75068	AAW75068 Enterobac
7	1091	93.0	249	AAW06463	AAW06463 Escherich
8	1091	93.0	249	AAW71029	AAW71029 Acid phos
9	1091	93.0	249	AAW75064	AAW75064 Escherich
10	1084	92.4	231	AAW71034	AAW71034 Mutant ac
11	1079	92.0	231	AAW71035	AAW71035 Mutant ac
12	1062	90.5	231	AAW71036	AAW71036 Mutant ac
13	1056	90.0	231	AAW71037	AAW71037 Mutant ac
14	1053	89.8	231	AAW71038	AAW71038 Mutant ac
15	1051	89.6	231	AAW71040	AAW71040 Mutant ac
16	1051	89.6	231	AAW71042	AAW71042 Mutant ac
17	1048	89.3	231	AAW71039	AAW71039 Mutant ac
18	1047	89.3	231	AAW71041	AAW71041 Mutant ac
19	1035	88.2	248	AAW06457	AAW06457 Providenc
20	1035	88.2	248	AAW71030	AAW71030 Acid phos
21	983.5	83.8	249	AAW06462	AAW06462 Morganell
22	983.5	83.8	249	AAW71028	AAW71028 Acid phos
23	983.5	83.8	249	AAW75065	AAW75065 Morganell
24	983.5	83.8	249	AAW27583	AAW27583 Fusion pr
25	772	65.8	244	AAW06460	AAW06460 Serratia

26	772	65.8	244	2	AAW71033	AAW71033 Acid phos
27	574.5	49.0	246	2	AAW54082	AAW54082 Virulence
28	569.5	48.6	246	2	AAW35759	AAW35759 Amylase (
29	475	40.5	232	4	AAW75066	AAW75066 Salmonell
30	341.5	29.1	264	4	AAW75067	AAW75067 Zygomonas
31	317	27.0	252	2	AAW20014	AAW20014 Ascorbic
32	193.5	16.5	943	8	ADL05772	ADL05772 M. catarr
33	191.5	16.3	428	7	ABO64424	ABO64424 Klebsiell
34	166	14.2	253	7	ABO79811	ABO79811 Pseudomon
35	165	14.1	585	8	ADG32050	ADG32050 Mutant B-
36	165	14.1	594	8	ADG32068	ADG32068 Mutant B-
37	153	13.0	987	7	ADP07500	ADP07500 Bacterial
38	149.5	12.7	508	4	AAW56365	AAW56365 Propionib
39	149.5	12.7	508	6	ABW52884	ABW52884 Propionib
40	135	11.5	513	5	ABP65275	ABP65275 Bifidobac
41	133	11.3	622	4	AAW91063	AAW91063 C. glutami
42	133	11.3	622	7	ADW87369	ADW87369 DNA repli
43	106.5	9.1	201	7	ADM26585	ADM26585 Hyperther
44	105	9.0	58	5	ABP08795	ABP08795 Human ORF
45	96	8.2	178	6	ABU49566	ABU49566 Protein e

ALIGNMENTS

RESULT 1	AAW06458	standard; protein; 248 AA.
ID	AAW06458	standard; protein; 248 AA.
AC	AAW06458;	
XX		
DT	13-AUG-1997	(first entry)
XX		
DE	Enterobacter aerogenes IFO 12010 acid phosphatase.	
XX		
KW	IFO 12010; acid phosphatase; production; nucleoside; 5'-phosphate; ester; condiment; pharmaceutical; intermediate.	
XX		
OS	Enterobacter aerogenes.	
XX		
FH	Key	Location/Qualifiers
FT	Misc-difference 92	/note="optionally replaced by another amino acid"
FT	Misc-difference 171	/note="optionally replaced by another amino acid"
FT	Misc-difference 171	/note="optionally replaced by another amino acid"
XX		
PN	WO9637603-A1.	
XX		
PD	28-NOV-1996.	
XX		
PF	24-MAY-1996;	96WO-JP001402.
XX		
PR	25-MAY-1995;	95JP-00149781.
XX		
PR	26-MAR-1996;	96JP-00094680.
XX		
PA	(AJIN) AJINOMOTO CO INC.	
XX		
PI	Mihara Y, Uragawa T, Yamada H, Asano Y;	
XX		
DR	WPI; 1997-021215/02.	
XX		
DR	N-Psdb; AAT45007.	
XX		
PT	Efficient production of nucleoside 5'-phosphate - by reaction of a nucleoside with a phosphoric acid donor in the presence of an acid phosphatase.	
XX		
PS	Claim 3; Page 67-68; 95pp; Japanese.	
XX		
CC	The present sequence is the Enterobacter aerogenes IFO 12010 acid phosphatase (AP), which can be used to produce a nucleoside 5'-phosphate ester from the corresponding nucleoside when a phosphate donor, e.g. poly-, phenyl- or carbamyl-phosphoric acid, is reacted in its presence at pH 3.0 to 5.5. The PA can be used for the economic and efficient production	

CC of nucleoside 5'-phosphate esters for use as condiments, pharmaceuticals
 CC and intermediates for pharmaceuticals
 CC
 SQ Sequence 248 AA;

Query Match 100.0%; Score 1173; DB 2; Length 248;
 Best Local Similarity 100.0%; Pred. No. 1.5e-118;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVPAAGNDATTKPDLYYLKNAQAIDSLALPPPEVGSIAFLNDQAMYEKGRLLRNTERGK 60
 DB 21 LVPAAGNDATTKPDLYYLKNAQAIDSLALPPPEVGSIAFLNDQAMYEKGRLLRNTERGK 80
 QY 61 LAADANLSAGVANAFASSAFSGSPITEKAPOLHKLITNMIEDAGDLATRSAXEKYMRIR 120
 DB 81 LAADANLSAGVANAFASSAFSGSPITEKAPOLHKLITNMIEDAGDLATRSAXEKYMRIR 140
 QY 121 PFAFYGVSTCNTTEODKLSKNGSPSGHTSIGMATLVLAELINPQRONEILKRGYELGES 180
 DB 141 PFAFYGVSTCNTTEODKLSKNGSPSGHTSIGMATLVLAELINPQRONEILKRGYELGES 200
 QY 181 RVICGYHMQSDVDARIVGSANVAVATLHTNPAFOOOLQKXDEFKATOK 228
 DB 201 RVICGYHMQSDVDARIVGSANVAVATLHTNPAFOOOLQKXDEFKATOK 248

RESULT 2

AAW71031
 ID AAW71031 standard; protein; 248 AA.

AC AAW71031;
 DT 21-OCT-1998. (first entry)

DE Acid phosphatase enzyme amino acid sequence.
 KW Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
 KM intermediate.
 OS Enterobacter aerogenes.

PN EP857788-A2.
 PD 12-AUG-1998.

PF 20-NOV-1997; 97EP-00309365.
 PR 21-NOV-1996; 96UP-00311103.
 PX 18-JUN-1997; 97JP-00161674.

PA (AJIN) AJINOMOTO CO INC.

PI Mihara Y, Utagawa T, Yamada H, Asano Y;
 DR WPI; 1998-416010/36.
 DR N-PSDB; AAW43060.

PT Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
 with phosphate donor in presence of acid phosphatase - used as seasonings
 or pharmaceutical intermediates.

PS Example 23; Page 44; 83pp; English.

CC The present sequence represents an acid phosphatase enzyme. The
 CC specification describes a method for the preparation of nucleoside 5'-
 CC phosphate esters. The method comprises reacting a nucleoside with a
 CC phosphate donor at pH 3.0-5.5 in the presence of an acid phosphatase that
 CC has been altered to increase its affinity for the nucleoside and/or to
 CC increase its thermal stability, or in the presence of a microorganism
 CC for such an acid phosphatase. Nucleoside 5'-phosphates are useful as
 CC seasonings or pharmaceuticals or as intermediates for them

SQ Sequence 248 AA;

Query Match 100.0%; Score 1173; DB 2; Length 248;
 Best Local Similarity 100.0%; Pred. No. 1.5e-118;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVPAAGNDATTKPDLYYLKNAQAIDSLALPPPEVGSIAFLNDQAMYEKGRLLRNTERGK 60
 DB 21 LVPAAGNDATTKPDLYYLKNAQAIDSLALPPPEVGSIAFLNDQAMYEKGRLLRNTERGK 80
 QY 61 LAADANLSAGVANAFASSAFSGSPITEKAPOLHKLITNMIEDAGDLATRSAXEKYMRIR 120
 DB 81 LAADANLSAGVANAFASSAFSGSPITEKAPOLHKLITNMIEDAGDLATRSAXEKYMRIR 140
 QY 121 PFAFYGVSTCNTTEODKLSKNGSPSGHTSIGMATLVLAELINPQRONEILKRGYELGES 180
 DB 141 PFAFYGVSTCNTTEODKLSKNGSPSGHTSIGMATLVLAELINPQRONEILKRGYELGES 200
 QY 181 RVICGYHMQSDVDARIVGSANVAVATLHTNPAFOOOLQKXDEFKATOK 228
 DB 201 RVICGYHMQSDVDARIVGSANVAVATLHTNPAFOOOLQKXDEFKATOK 248

RESULT 3

ABO61416
 ID ABO61416 standard; protein; 253 AA.

AC ABO61416;

DT 29-JUL-2004 (first entry)

DE Klebsiella pneumoniae polypeptide seqid 7933.

KW Recombinant expression vector; transcription regulatory element;
 KM Klebsiella pneumoniae protein; antibacterial; vaccine.
 OS Klebsiella pneumoniae.

PN US6610836-B1.

PD 26-AUG-2003.

PF 27-JAN-2000; 2000US-00489039.

PR 29-JAN-1999; 99US-0117747P.

PA (GENO-) GENOME THERAPEUTICS CORP.

PI Breton GL, Osborne M;

DR WPI; 2003-895346/82.

DR N-PSDB; ACH94967.

PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
 preparing a vaccine composition against Klebsiella pneumoniae.

PS Disclosure; SEQ ID NO 7933; 932pp; English.

CC The invention describes a new isolated nucleic acid encoding a Klebsiella
 CC pneumoniae polypeptide. Also described are: a recombinant expression
 CC vector comprising the nucleic acid, operably linked to a transcription
 CC regulatory element; and a cell comprising the recombinant expression
 CC vector. The nucleic acid is useful for preparing a vaccine composition
 CC against Klebsiella pneumoniae. This is the amino acid sequence of a
 CC Klebsiella pneumoniae polypeptide of the invention

SQ Sequence 253 AA;

Query Match 97.1%; Score 1139; DB 7; Length 253;
 Best Local Similarity 96.9%; Pred. No. 7.9e-115;
 Matches 221; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 LVPAAGNDATTKPDLYYLKNAQAIDSLALPPPEVGSIAFLNDQAMYEKGRLLRNTERGK 60

Best Local Similarity 96.9%; Pred. No. 1,66-114;
Matches 221; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 LVPAAGNDATTKPDLYYLKNAQAIDSLALLPPPEVGSIAFLNDQAMYEKGRLLRNTERGK 60
Db 21 LVPAAGNDATTKPDLYYLKNAQAIDSLALLPPPEVGSIAFLNDQAMYEKGRLLRNTERGK 80
QY 61 LAAEDANLSAGVANAFAFSAPFSPITEKDAPOHLKLLTNMTEDAGDLATRSAREKYMIR 120
Db 81 LAAEDANLSAGVANAFAFSAPFSPITEKDAPOHLKLLTNMTEDAGDLATRSAREKYMIR 140
QY 121 PPAFYGVSTCNTTEODKLSKNGSYSPGHTSIGMATLVLAELINPORONEILKRGYEIGES 180
Db 141 PPAFYGVSTCNTTEODKLSKNGSYSPGHTSIGMATLVLAELINPORONEILKRGYEIGES 200
QY 181 RVICGYHMQSDVDARIVGSAVVATLHTNPAFOOOLQKAKDEPAKTOK 228
Db 201 RVICGYHMQSDVDARIVGSAVVATLHTNPAFOOOLQKAKDEPAKTOK 248

RESULT 6

AAB75068
ID AAB75068 standard; protein; 248 AA.
XX AAB75068;

DT 23-JUL-2001 (first entry)
XX

DE Enterobacter aerogenes nucleoside-5'-phosphate producing enzyme protein.

KM Variant nucleoside-5'-phosphate producing enzyme; mutagenesis;
KM transphosphorylation; phosphate; protein co-ordinate data;
XX X-ray structural analysis; three-dimensional structure.

OS Enterobacter aerogenes.

XX MO200118184-A1.

XX 15-MAR-2001.

PD 01-SEP-2000; 2000WO-JP005973.

XX 03-SEP-1999; 99JP-00249545.

PA (AJIN) AJINOMOTO CO INC.

PI Ishikawa K, Suzuki E, Gondoh K, Shimba N, Mihara Y, Kawasaki H,
PI Kurahashi O, Kouda T, Shimaoka M, Kozutsumi R, Asano Y;

DR WPI; 2001-380914/40.

DR N-PSDB; AAH19705.

PT Variant enzyme having elevated nucleoside 5'-prime phosphate producing
PT activity and having a specific three-dimensional structure for production
of nucleosides as pharmaceutical intermediates.

XX Example 19; Page 117-118; 150pp; Japanese.

CC The present invention describes a variant nucleoside-5'-phosphate
CC producing enzyme which is a modification of a transphosphorylase or
CC phosphatase which contains a lysine, two arginine and two histidine
CC residues and in which the C-alpha distances between these residues are
CC enclosing a space which permits the binding of a nucleoside with these
CC residues. Also described are: (1) a gene encoding the variant enzyme; (2)
CC expression vectors containing the DNA; (3) host cells transformed by the
CC vectors; (4) preparation of the variant enzyme by culture of the
CC transformants; (5) crystals of the enzyme and of a complex of the enzyme
CC with molybdenic acid; and (6) selection of inhibitors of acid phosphatase
CC or transphosphorylase using the structural coordinates derived from the
CC enzyme. The variant enzymes with increased efficiency for production of
CC nucleoside 5'-phosphates can be used as pharmaceutical intermediates.
CC AAH19701 to AAH19785 and AAB75064 to AAB75101 represent sequences used in
CC the exemplification of the present invention

XX SQ Sequence 248 AA;

Query Match 96.1%; Score 1127; DB 4; Length 248;
Best Local Similarity 96.1%; Pred. No. 1,66-113;
Matches 219; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 LVPAAGNDATTKPDLYYLKNAQAIDSLALLPPPEVGSIAFLNDQAMYEKGRLLRNTERGK 60
Db 21 LVPAAGNDATTKPDLYYLKNAQAIDSLALLPPPEVGSIAFLNDQAMYEKGRLLRNTERGK 80
QY 61 LAAEDANLSAGVANAFAFSAPFSPITEKDAPOHLKLLTNMTEDAGDLATRSAREKYMIR 120
Db 81 OQADADLAAGVANAFAFSAPFSPITEKDAPOHLKLLTNMTEDAGDLATRSAREKYMIR 140
QY 121 PPAFYGVSTCNTTEODKLSKNGSYSPGHTSIGMATLVLAELINPORONEILKRGYEIGES 180
Db 141 PPAFYGVSTCNTTKDDKLSKNGSYSPGHTSIGMATLVLAELINPORONEILKRGYEIGES 200
QY 181 RVICGYHMQSDVDARIVGSAVVATLHTNPAFOOOLQKAKDEPAKTOK 228
Db 201 RVICGYHMQSDVDARIVGSAVVATLHTNPAFOOOLQKAKDEPAKTOK 248

RESULT 7

AAW06463
ID AAW06463 standard; protein; 249 AA.

XX AAW06463;

DT 13-AUG-1997 (first entry)
XX

DE Escherichia blattae JCM 1650 acid phosphatase.

KM JCM 1650; acid phosphatase; production; nucleoside; 5'-phosphate; ester;
KM condiment; pharmaceutical; intermediate.

XX Escherichia blattae.

XX Key Location/Qualifiers
FT Peptide 1..18
FT Peptide /label= sig_peptide
FT Peptide 19..249
FT /label= mat_peptide

FT Misc-difference 92

FT /note= "optionally replaced by another amino acid"

FT Misc-difference 171
FT /note= "optionally replaced by another amino acid"

XX MO9637603-A1.

XX 28-NOV-1996.

PD 24-MAY-1996; 96WO-JP001402.

XX 25-MAY-1995; 95JP-00149781.

XX 26-MAR-1996; 96JP-00094680.

PA (AJIN) AJINOMOTO CO INC.

PI Mihara Y, Utagawa T, Yamada H, Asano Y;

DR WPI; 1997-021215/02.

DR N-PSDB; AAT45011.

PT Efficient production of nucleoside 5'-phosphate - by reaction of a
PT nucleoside with a phosphoric acid donor in the presence of an acid
PT phosphatase.

XX Claim 3; Page 56-58; 95pp; Japanese.

CC The present sequence is the Escherichia blattae JCM 1650 acid phosphatase
CC (AP), which can be used to produce a nucleoside 5'-phosphate ester from

CC the corresponding nucleoside when a phosphate donor, e.g. poly-, phenyl-,
CC or carboxy-1-phosphoric acid, is reacted in its presence at pH 3.0 to 5.5.
CC The PA can be used for the economic and efficient production of
CC nucleoside 5'-phosphate esters for use as condiments, pharmaceuticals and
CC intermediates for pharmaceuticals

XX Sequence 249 AA;

SO Query Match 93.0%; Score 1091; DB 2; Length 249;

Best Local Similarity 92.1%; Pred. No. 1.3e-109; Indels 0; Gaps 0;

Matches 210; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 LVPAAGNDATTPKPDLYLLKNAQAIDSLALPPPEVGSIAFLNDQAMYEKGLRTERGK 60

DB 21 LVATGNDTTTPKPDLYLLKNSSEALNSLALPPPAVGSIAFLNDQAMYEKGLRTERGK 80

QY 61 LAEDANLSAGGVANAFSGAFSGPTEKDAFOLHKLNTMIEDAGDLATRSKAKHYMRIR 120

DB 81 LAEDANLSAGGVANAFSGAFSGPTEKDAFOLHKLNTMIEDAGDLATRSKAKHYMRIR 140

QY 121 PPAFYGSTCNTTEBODKLSKNGSPSGHTSIGMATLVLAIEINPORONEILKRGYELGS 180

DB 141 PPAFYGSTCNTTEBODKLSKNGSPSGHTSIGMATLVLAIEINPORONEILKRGYELGS 200

QY 181 RVICGYHWSQSDVDARIVGSAAVATLHTNPAFOOLQKAKDEFKATOK 228

DB 201 RVICGYHWSQSDVDARIVGSAAVATLHTNPAFOOLQKAKDEFKATOK 248

RESULT 8

AAM71029 AAM71029 standard; protein; 249 AA.

XX AAM71029;

DT 21-OCT-1998 (first entry)

DE Acid phosphatase enzyme amino acid sequence.

XX Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;

KM intermediate.

XX Escherichia blattae.

OS Key Location/Qualifiers

FT Peptide 1..18 /note= "signal peptide"

FT Protein 19..249 /note= "mature protein; Claim 6"

XX EP857788-A2.

PD 12-AUG-1998.

PF 20-NOV-1997; 97EP-00309365.

PR 21-NOV-1996; 96JP-00311103.

PR 18-JUN-1997; 97JP-00161674.

PA (AJIN) AJINOMOTO CO INC.

PI Mihara Y, Utagawa T, Yamada H, Asano Y;

DR N-PSDB; AA43046.

XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside

PT with phosphate donor in presence of acid phosphatase - used as seasonings

XX or pharmaceutical intermediates.

PS Example 12; Page 35-36; 83pp; English.

XX The present sequence represents an acid phosphatase enzyme. The

CC specification describes a method for the preparation of nucleoside 5'-
CC phosphate esters. The method comprises reacting a nucleoside with a
CC phosphate donor at pH 3.0-5.5 in the presence of an acid phosphatase that
CC has been altered to increase its affinity for the nucleoside and/or to
CC increase its thermal stability, or in the presence of a microorganism
CC that has been transformed with recombinant DNA containing a gene coding
CC for such an acid phosphatase. Nucleoside 5'-phosphates are useful as
CC seasonings or pharmaceuticals or as intermediates for them

XX Sequence 249 AA;

SO Query Match 93.0%; Score 1091; DB 2; Length 249;

Best Local Similarity 92.1%; Pred. No. 1.3e-109; Indels 0; Gaps 0;

Matches 210; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 LVPAAGNDATTPKPDLYLLKNAQAIDSLALPPPEVGSIAFLNDQAMYEKGLRTERGK 60

DB 21 LVATGNDTTTPKPDLYLLKNSSEALNSLALPPPAVGSIAFLNDQAMYEKGLRTERGK 80

QY 61 LAEDANLSAGGVANAFSGAFSGPTEKDAFOLHKLNTMIEDAGDLATRSKAKHYMRIR 120

DB 81 LAEDANLSAGGVANAFSGAFSGPTEKDAFOLHKLNTMIEDAGDLATRSKAKHYMRIR 140

QY 121 PPAFYGSTCNTTEBODKLSKNGSPSGHTSIGMATLVLAIEINPORONEILKRGYELGS 180

DB 141 PPAFYGSTCNTTEBODKLSKNGSPSGHTSIGMATLVLAIEINPORONEILKRGYELGS 200

QY 181 RVICGYHWSQSDVDARIVGSAAVATLHTNPAFOOLQKAKDEFKATOK 228

DB 201 RVICGYHWSQSDVDARIVGSAAVATLHTNPAFOOLQKAKDEFKATOK 248

RESULT:9

AAB75064 AAB75064 standard; protein; 249 AA.

XX AAB75064;

DT 23-JUN-2001 (first entry)

DE Escherichia blattae nucleoside-5'-phosphate producing enzyme protein.

XX Variant nucleoside-5'-phosphate producing enzyme; mutagenesis;

KM transphosphorylation; phosphate; protein co-ordinate data;

XX X-ray structural analysis; three-dimensional structure.

OS Escherichia blattae.

PN WO200118184-A1.

PD 15-MAR-2001.

PF 01-SEP-2000; 2000WO-JP005973.

PR 03-SEP-1999; 99JP-00249545.

PA (AJIN) AJINOMOTO CO INC.

PI Ishikawa K, Suzuki E, Gondoh K, Shimba N, Mihara Y, Kawasaki H;

PI Kurahashi O, Kouda T, Shimooka M, Kozutsumi R, Asano Y;

DR N-PSDB; AA419701.

XX Variant enzyme having elevated nucleoside 5'-prime phosphate producing

PT activity and having a specific three-dimensional structure for production

XX of nucleosides as pharmaceutical intermediates.

PS Disclosure; Page 107; 150pp; Japanese.

XX The present invention describes a variant nucleoside-5'-phosphate

CC producing enzyme which is a modification of a transphosphorylase or

CC phosphatase which contains a lysine, two arginine and two histidine

CC residues and in which the C-alpha distances between these residues are
CC enclosing a space which permits the binding of a nucleoside with these
CC residues. Also described are: (1) a gene encoding the variant enzyme; (2)
CC expression vectors containing the DNA; (3) host cells transformed by the
CC vectors; (4) preparation of the variant enzyme by culture of the
CC transformants; (5) crystals of the enzyme and of a complex of the enzyme
CC with molybdenic acid; and (6) selection of inhibitors of acid phosphatase
CC or transphosphorylase using the structural coordinates derived from the
CC enzyme. The variant enzymes can be used as pharmaceutical intermediates.
CC AAH19701 to AAH19785 and AAB75064 to AAB75101 represent sequences used in
CC the exemplification of the present invention
XX
SQ Sequence 249 AA;
Query Match 93.0%; Score 1091; DB 4; Length 249;
Best Local Similarity 92.1%; Pred. No. 1.3e-109;
Matches 210; Conservative 9; Mismatches 9; Indels 0; Gaps 0;
QY 1 LVPAGNDATTTPDLYLLKNAQAIDSLALLPPPEVSGIAFLNDQAMTEKGLLNTTERGK 60
DB 21 LVATGNDTTTPDLYLLKNSAIDSLALLPPPAVGSIAFLNDQAMTEQGLLNTTERGK 80
QY 61 LAEDANLSAGVANAFAFGSPITEKDAFOLHKLITNMIEDAGDLATRSAREKYMIR 120
DB 81 LAEDANLSAGVANAFAFGSPITEKDAFOLHKLITNMIEDAGDLATRSADHYMRIR 140
QY 121 PFAFYGVSTCNTTEODPLSKNGSYPSGHTSIGWATLVALEINPQRONEILKRGYEIGES 180
DB 141 PFAFYGVSTCNTTEODPLSKNGSYPSGHTSIGWATLVALEINPQRONEILKRGYELGOS 200
QY 181 RVICGYHMQSDVDAAIRVGSAAVVALTHTNPAFOQOLOKADEFAKTOK 228
DB 201 RVICGYHMQSDVDAAIRVGSAAVVALTHTNPAFOQOLOKADEFAKCHQK 248
RESULT 10
AAW71034
ID AAW71034 standard; protein; 231 AA.
AC AAW71034;
XX
XX
DT 21-OCT-1998 (first entry)
XX
DE Mutant acid phosphatase enzyme of *Escherichia* blattae.
XX
KW Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
XX mutant; intermediate.
XX
OS Synthetic.
XX *Escherichia* blattae.
XX
FH Key Location/Qualifiers
FT Misc-difference 74
FT /label= G74D
XX
XX
PN EP857788-A2.
XX
PD 12-AUG-1998.
XX
PF 20-NOV-1997; 97EP-00309365.
XX
PR 21-NOV-1996; 96JP-00311103.
PR 18-JUN-1997; 97JP-00161674.
XX
XX (AJIN) AJINOMOTO CO INC.
XX
XX Mihara Y, Utagawa T, Yamada H, Asano Y;
XX WPI, 1998-416010/36.
XX
XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
XX with phosphate donor in presence of acid phosphatase - used as seasonings
XX

PT or pharmaceutical intermediates.
XX
XX Example 19; Page; 83pp; English.
PS
XX
XX AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
CC created using the mature protein of AAW71029. The specification describes
CC a method for the preparation of nucleoside 5'-phosphate esters. The
CC method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
CC 5.5 in the presence of an acid phosphatase that has been altered to
CC increase its affinity for the nucleoside and/or to increase its thermal
CC stability, or in the presence of a microorganism that has been
CC transformed with recombinant DNA containing a gene coding for such an
CC acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
CC pharmaceuticals or as intermediates for them. note: this sequence does
CC not appear in the specification; it was created using information
XX provided
XX
SQ Sequence 231 AA;
Query Match 92.4%; Score 1084; DB 2; Length 231;
Best Local Similarity 91.7%; Pred. No. 6.6e-109;
Matches 209; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
QY 1 LVPAGNDATTTPDLYLLKNAQAIDSLALLPPPEVSGIAFLNDQAMTEKGLLNTTERGK 60
DB 3 LVATGNDTTTPDLYLLKNSAIDSLALLPPPAVGSIAFLNDQAMTEQGLLNTTERGK 62
QY 61 LAEDANLSAGVANAFAFGSPITEKDAFOLHKLITNMIEDAGDLATRSAREKYMIR 120
DB 63 LAEDANLSAGVANAFAFGSPITEKDAFOLHKLITNMIEDAGDLATRSADHYMRIR 122
QY 121 PFAFYGVSTCNTTEODPLSKNGSYPSGHTSIGWATLVALEINPQRONEILKRGYEIGES 180
DB 123 PFAFYGVSTCNTTEODPLSKNGSYPSGHTSIGWATLVALEINPQRONEILKRGYELGOS 182
QY 181 RVICGYHMQSDVDAAIRVGSAAVVALTHTNPAFOQOLOKADEFAKTOK 228
DB 183 RVICGYHMQSDVDAAIRVGSAAVVALTHTNPAFOQOLOKADEFAKCHQK 230
RESULT 11
AAW71035
ID AAW71035 standard; protein; 231 AA.
AC AAW71035;
XX
XX
DT 21-OCT-1998 (first entry)
XX
DE Mutant acid phosphatase enzyme of *Escherichia* blattae.
XX
KW Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
XX mutant; intermediate.
XX
OS Synthetic.
XX *Escherichia* blattae.
XX
FH Key Location/Qualifiers
FT Misc-difference 74
FT /label= G74D
FT Misc-difference 153
FT /label= I153T
XX
XX
PN EP857788-A2.
XX
PD 12-AUG-1998.
XX
PF 20-NOV-1997; 97EP-00309365.
XX
XX
XX 21-NOV-1996; 96JP-00311103.
XX 18-JUN-1997; 97JP-00161674.
XX
XX (AJIN) AJINOMOTO CO INC.
XX

PI Mihara Y, Utagawa T, Yamada H, Asano Y;
 XX
 XX WPI, 1998-416010/36.
 XX
 PT Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
 FT with phosphate donor in presence of acid phosphatase - used as seasonings
 PT or pharmaceutical intermediates.
 XX
 PS Example 19; Page: 83pp; English.
 XX
 CC AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
 CC created using the mature protein of AAW71029. The specification describes
 CC a method for the preparation of nucleoside 5'-phosphate esters. The
 CC method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
 CC 5.5 in the presence of an acid phosphatase that has been altered to
 CC increase its affinity for the nucleoside and/or to increase its thermal
 CC stability, or in the presence of a microorganism that has been
 CC transformed with recombinant DNA containing a gene coding for such an
 CC acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
 CC pharmaceuticals or as intermediates for them. note: this sequence does
 CC not appear in the specification; it was created using information
 CC provided
 CC
 XX
 SQ Sequence 231 AA;
 Query Match 92.0%; Score 1079; DB 2; Length 231;
 Best Local Similarity 91.2%; Pred. No. 2.3e-108;
 Matches 208; Conservative 9; Mismatches 11; Indels 0; Gaps 0;
 QY 1 LVPAGNDATTPKEDLYLNNQAQIDSLALLPPEVGSIAFLNDQMYEGRLLRNTERRG 60
 DB 3 LVATGNDTTTKPDLYLNNSEAINSLALLPPPAVGSIAFLNDQMYEGRLLRNTERRG 62
 QY 61 LAEDPANSAGVANAFASSAFSPITEKDAPOHLKLTMTMIDADDLATRSKDEKYMIR 120
 DB 63 LAEDPANSISGDVANAFAFGAFSPITEKDAPOHLKLTMTMIDADDLATRSKDEKYMIR 122
 QY 121 PPAFYGVSTCNTTEBODKLSKNGSYPSGHTSIGMATALVLAETINPORONEILKRGYELGES 180
 DB 123 PPAFYGVSTCNTTEBODKLSKNGSYPSGHTSIGMATALVLAETINPORONEILKRGYELGES 182
 QY 181 RVICGYHMQSDVDAAARIVGSAVVATLHTNPAFOQLQAKDEFAKQK 228
 DB 183 RVICGYHMQSDVDAAARIVGSAVVATLHTNPAFOQLQAKDEFAKQK 230
 RESULT 12
 AAW71036
 ID AAW71036 standard; protein; 231 AA.
 XX
 AC AAW71036;
 XX
 DT 21-OCT-1998 (first entry)
 XX
 DE Mutant acid phosphatase enzyme of Escherichia blattae.
 XX
 KM Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
 KM mutant; intermediate.
 XX
 OS Synthetic.
 OS Escherichia blattae.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 63
 FT Misc-difference /label= L63Q
 FT Misc-difference 65
 FT Misc-difference /label= A65Q
 FT Misc-difference 66
 FT Misc-difference /label= E66A
 FT Misc-difference 74
 FT Misc-difference /label= G74D
 FT Misc-difference 153
 FT Misc-difference /label= I153T

XX
 PN EP857788-A2.
 XX
 PD 12-AUG-1998.
 XX
 PF 20-NOV-1997; 97EP-00309365.
 XX
 PR 21-NOV-1996; 96JP-00311103.
 XX
 PR 18-JUN-1997; 97JP-00161674.
 XX
 PA (AJTN) AJINOMOTO CO INC.
 XX
 PI Mihara Y, Utagawa T, Yamada H, Asano Y;
 XX
 XX WPI, 1998-416010/36.
 XX
 DR
 XX
 PT Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
 FT with phosphate donor in presence of acid phosphatase - used as seasonings
 PT or pharmaceutical intermediates.
 XX
 PS Example 19; Page: 83pp; English.
 XX
 CC AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
 CC created using the mature protein of AAW71029. The specification describes
 CC a method for the preparation of nucleoside 5'-phosphate esters. The
 CC method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
 CC 5.5 in the presence of an acid phosphatase that has been altered to
 CC increase its affinity for the nucleoside and/or to increase its thermal
 CC stability, or in the presence of a microorganism that has been
 CC transformed with recombinant DNA containing a gene coding for such an
 CC acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
 CC pharmaceuticals or as intermediates for them. note: this sequence does
 CC not appear in the specification; it was created using information
 CC provided
 CC
 XX
 SQ Sequence 231 AA;
 Query Match 90.5%; Score 1062; DB 2; Length 231;
 Best Local Similarity 89.9%; Pred. No. 1.6e-106;
 Matches 205; Conservative 9; Mismatches 14; Indels 0; Gaps 0;
 QY 1 LVPAGNDATTPKEDLYLNNQAQIDSLALLPPEVGSIAFLNDQMYEGRLLRNTERRG 60
 DB 3 LVATGNDTTTKPDLYLNNSEAINSLALLPPPAVGSIAFLNDQMYEGRLLRNTERRG 62
 QY 61 LAEDPANSAGVANAFASSAFSPITEKDAPOHLKLTMTMIDADDLATRSKDEKYMIR 120
 DB 63 QAODPANSISGDVANAFAFGAFSPITEKDAPOHLKLTMTMIDADDLATRSKDEKYMIR 122
 QY 121 PPAFYGVSTCNTTEBODKLSKNGSYPSGHTSIGMATALVLAETINPORONEILKRGYELGES 180
 DB 123 PPAFYGVSTCNTTEBODKLSKNGSYPSGHTSIGMATALVLAETINPORONEILKRGYELGES 182
 QY 181 RVICGYHMQSDVDAAARIVGSAVVATLHTNPAFOQLQAKDEFAKQK 228
 DB 183 RVICGYHMQSDVDAAARIVGSAVVATLHTNPAFOQLQAKDEFAKQK 230
 RESULT 13
 AAW71037
 ID AAW71037 standard; protein; 231 AA.
 XX
 AC AAW71037;
 XX
 DT 21-OCT-1998 (first entry)
 XX
 DE Mutant acid phosphatase enzyme of Escherichia blattae.
 XX
 KM Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
 KM mutant; intermediate.
 XX
 OS Synthetic.
 OS Escherichia blattae.

```

XX Key Location/Qualifiers
FH Misc-difference 63 /label= L63Q
FT Misc-difference 65 /label= A65Q
FT Misc-difference 66 /label= E66A
FT Misc-difference 74 /label= G74D
FT Misc-difference 85 /label= S85Y
FT Misc-difference 153 /label= I153T
FT EP857788-A2.
XX 12-AUG-1998.
XX 20-NOV-1997; 97EP-00309365.
XX 21-NOV-1996; 96JP-00311103.
XX 18-JUN-1997; 97JP-00161674.
XX (AJTN) AJINOMOTO CO INC.
XX Mihara Y, Utagawa T, Yamada H, Asano Y;
XX WPI; 1998-416010/36.
XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
XX with phosphate donor in presence of acid phosphatase - used as seasonings
XX or pharmaceutical intermediates.
XX Example 19; Page; 83pp; English.
XX AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
XX created using the mature protein of AAW71029. The specification describes
XX a method for the preparation of nucleoside 5'-phosphate esters. The
XX method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
XX 5.5 in the presence of an acid phosphatase that has been altered to
XX increase its affinity for the nucleoside and/or to increase its thermal
XX stability, or in the presence of a microorganism that has been
XX transformed with recombinant DNA containing a gene coding for such an
XX acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
XX pharmaceuticals or as intermediates for them. note: this sequence does
XX not appear in the specification; it was created using information
XX provided
XX
XX Sequence 231 AA;

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Query Match 90.0%; Score 1056; DB 2; Length 231;
Best Local Similarity 89.5%; Pred. No. 7.4e-106;
Matches 204; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
DB 1 LVAGNDATTKPLLYIKNAQIDSLALPPPEVGSIAFLINDQAMYEKGRLLRTERGX 60
QY 1 LVAGNDATTKPLLYIKNAQIDSLALPPPEVGSIAFLINDQAMYEKGRLLRTERGX 60
DB 3 LVATGNDTTPKPLLYIKNAQIDSLALPPPEVGSIAFLINDQAMYEKGRLLRTERGX 62
QY 1 LAEDNLSAGVANAFFSFAFGSPITEKDAFOLHKLITNMIEDAGLATRSANEKYMIR 120
DB 61 QAOQADNLSGGDVANAFSFAFGSPITEKDAFOLHKLITNMIEDAGLATRSANEKYMIR 122
QY 63 QAOQADNLSGGDVANAFSFAFGSPITEKDAFOLHKLITNMIEDAGLATRSANEKYMIR 122
DB 121 PFAFYGVSTCNTTEODKLSKNGSYPSGHSISGAWATLVLAETIPORONELIKRGYLGSS 180
QY 123 PFAFYGVSTCNTTEODKLSKNGSYPSGHSISGAWATLVLAETIPORONELIKRGYLGSS 182
DB 181 RVICGHWOSDVDAARVGSAAVATLHTNPAFOOQLOKADERAKTOK 228
QY 183 RVICGHWOSDVDAARVGSAAVATLHTNPAFOOQLOKADERAKTOK 230

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RESULT 14

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AAW71038
ID AAW71038 standard; protein; 231 AA.
XX
XX AAW71038;
AC 21-OCT-1998 (first entry)
XX
XX Mutant acid phosphatase enzyme of Escherichia blattae.
XX
XX Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
XX mutant; intermediate.
XX Synthetic.
XX Escherichia blattae.
XX
XX Key Location/Qualifiers
FH Misc-difference 63 /label= L63Q
FT Misc-difference 65 /label= A65Q
FT Misc-difference 66 /label= E66A
FT Misc-difference 74 /label= G74D
FT Misc-difference 135 /label= T135K
FT Misc-difference 136 /label= E136D
FT Misc-difference 153 /label= I153T
FT EP857788-A2.
XX 12-AUG-1998.
XX 20-NOV-1997; 97EP-00309365.
XX 21-NOV-1996; 96JP-00311103.
XX 18-JUN-1997; 97JP-00161674.
XX (AJTN) AJINOMOTO CO INC.
XX Mihara Y, Utagawa T, Yamada H, Asano Y;
XX WPI; 1998-416010/36.
XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
XX with phosphate donor in presence of acid phosphatase - used as seasonings
XX or pharmaceutical intermediates.
XX Example 19; Page; 83pp; English.
XX AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
XX created using the mature protein of AAW71029. The specification describes
XX a method for the preparation of nucleoside 5'-phosphate esters. The
XX method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
XX 5.5 in the presence of an acid phosphatase that has been altered to
XX increase its affinity for the nucleoside and/or to increase its thermal
XX stability, or in the presence of a microorganism that has been
XX transformed with recombinant DNA containing a gene coding for such an
XX acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
XX pharmaceuticals or as intermediates for them. note: this sequence does
XX not appear in the specification; it was created using information
XX provided
XX
XX Sequence 231 AA;

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Query Match 89.8%; Score 1053; DB 2; Length 231;
Best Local Similarity 89.0%; Pred. No. 1.6e-105;
Matches 203; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
QY 1 LVAGNDATTKPLLYIKNAQIDSLALPPPEVGSIAFLINDQAMYEKGRLLRTERGX 60

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Db      3 LVATGNDTTTKPDLYLLKNSEAINSLALLPPPAVGSIAFLNDQAMVEQGRLLRNTTERGK 62
Qy      61 LAEPDANLSAGVNAFSSAFSGSPITTEKDAPOLHKLTLNMTEDAGDLATRSKKEKYMIR 120
Db      63 QOQADANLSSGDVNAFSGAFSGSPITTEKDAPALHKLTLNMTEDAGDLATRSKKEHYMRIR 122
Qy      121 PPAFYGVSTCNTTTEODKLSKNGSYSGHTSIGMATLVLAELINPORONEILKRGYELGGS 180
Db      123 PPAFYGVSTCNTKDDKLSKNGSYSGHTSIGMATLVLAELINPORONEILKRGYELGGS 182
Qy      181 RVICGYHMOSDVAARIYGSAAVATLHTNPAFOOQLQKAKDEFPAKTOK 228
Db      183 RVICGYHMOSDVAARIYGSAAVATLHTNPAFOOQLQKAKDEFPAQHOK 230

RESULT 15
AAW71040
ID      AAW71040 standard; protein; 231 AA.
XX      AC      AAW71040;
XX      DT      21-OCT-1998 (first entry)
DE      Mutant acid phosphatase enzyme of Escherichia blattae.
XX      KW      Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
XX      mutant; intermediate.
XX      OS      Synthetic.
XX      OS      Escherichia blattae.
FH      Key      Location/Qualifiers
FT      Misc-difference 63 /label= L63Q
FT      Misc-difference 65 /label= A65Q
FT      Misc-difference 66 /label= E66A
FT      Misc-difference 69 /label= N69D
FT      Misc-difference 71 /label= S71A
FT      Misc-difference 72 /label= S72A
FT      Misc-difference 74 /label= G74D
FT      Misc-difference 116 /label= D116E
FT      Misc-difference 135 /label= T135K
FT      Misc-difference 136 /label= E136D
FT      Misc-difference 153 /label= I153T
XX      PN      EP857788-A2.
XX      PD      12-AUG-1998.
XX      PF      20-NOV-1997; 97EP-00309365.
XX      PR      21-NOV-1996; 96JP-00311103.
XX      PR      18-JUN-1997; 97JP-00161674.
XX      PA      (AJIN ) AJINOMOTO CO INC.
XX      PI      Mihara Y, Utagawa T, Yamada H, Asano Y;
XX      DR      WPI; 1998-416010/36.
XX      PT      Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
XX      PT      with phosphate donor in presence of acid phosphatase - used as seasonings
XX      PT      or pharmaceutical intermediates.

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XX      XX      Example 19: Page; 83pp; English.
PS      CC      AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
XX      CC      created using the mature protein of AAW71029. The specification describes
XX      CC      a method for the preparation of nucleoside 5'-phosphate esters. The
XX      CC      method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
XX      CC      5.5 in the presence of an acid phosphatase that has been altered to
XX      CC      increase its affinity for the nucleoside and/or to increase its thermal
XX      CC      stability, or in the presence of a microorganism that has been
XX      CC      transformed with recombinant DNA containing a gene coding for such an
XX      CC      acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
XX      CC      pharmaceuticals or as intermediates for them. note: this sequence does
XX      CC      not appear in the specification; it was created using information
XX      CC      provided
XX      SQ      Sequence 231 AA;
XX      Query Match      89.6%; Score 1051; DB 2; Length 231;
XX      Best Local Similarity 89.0%; Pred. No. 2.6e-105;
XX      Matches 203; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
Qy      1 LVPAQNDATTYKPDLYLLKNQAIDSLALLPPPEVGSIAFLNDQAMYEKGRLLRNTTERGK 60
Db      3 LVATGNDTTTKPDLYLLKNSEAINSLALLPPPAVGSIAFLNDQAMVEQGRLLRNTTERGK 62
Qy      61 LAEPDANLSAGVNAFSSAFSGSPITTEKDAPOLHKLTLNMTEDAGDLATRSKKEKYMIR 120
Db      63 QOQADANLSSGDVNAFSGAFSGSPITTEKDAPALHKLTLNMTEDAGDLATRSKKEHYMRIR 122
Qy      121 PPAFYGVSTCNTTTEODKLSKNGSYSGHTSIGMATLVLAELINPORONEILKRGYELGGS 180
Db      123 PPAFYGVSTCNTKDDKLSKNGSYSGHTSIGMATLVLAELINPORONEILKRGYELGGS 182
Qy      181 RVICGYHMOSDVAARIYGSAAVATLHTNPAFOOQLQKAKDEFPAKTOK 228
Db      183 RVICGYHMOSDVAARIYGSAAVATLHTNPAFOOQLQKAKDEFPAQHOK 230

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Search completed: March 2, 2005, 20:22:55
Job time : 117.732 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 2, 2005, 20:15:06 ; Search time 113.255 Seconds
(without alignments)
1030.896 Million cell updates/sec

Title: US-09-807-990A-125
Perfect score: 1173
Sequence: 1 LVPAQNDAITKPDLYYLKNA.....NPAFOOOLQKAKDEFKATQK 228

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1173	100.0	248	2	Q9FIU1 enterobacte
2	1136	96.8	248	2	Q9FIU0 klebsiella
3	1108	94.5	248	2	Q9RIW6 klebsiella
4	1091	93.0	249	2	Q9SIA6 escherichia
5	1046	89.2	249	2	Q9SIA6 escherichia
6	1043	88.9	249	2	Q9SIA6 escherichia
7	1035	88.2	248	1	PHON PROST
8	983.5	83.8	249	1	PHOC MORMO
9	773	65.9	263	2	Q9SIA6 escherichia
10	579.5	49.4	246	2	Q9SIA6 escherichia
11	574.5	49.0	246	2	Q9SIA6 escherichia
12	573.5	48.9	246	2	Q9SIA6 escherichia
13	568.5	48.5	246	2	Q9SIA6 escherichia
14	495.5	42.2	280	2	Q9SIA6 escherichia
15	483	41.2	250	1	PHON SALTY
16	477.5	40.7	250	2	Q9SIA6 escherichia
17	476.5	40.6	250	2	Q9SIA6 escherichia
18	476.5	40.6	250	2	Q9SIA6 escherichia
19	474	40.4	250	2	Q9SIA6 escherichia
20	465.5	39.7	283	2	Q9SIA6 escherichia
21	464.5	39.7	280	2	Q9SIA6 escherichia
22	417.5	35.6	289	2	Q9SIA6 escherichia
23	341.5	29.1	264	1	PPA_ZYMO
24	274.5	23.4	258	2	Q9AB73 caulobacter
25	214	18.2	231	2	Q9AB73 caulobacter
26	189	16.1	423	2	Q9AB73 caulobacter
27	186	15.9	2314	2	Q9AB73 caulobacter
28	165	14.1	596	2	Q9AB73 caulobacter
29	161	13.7	596	2	Q9AB73 caulobacter
30	160	13.6	435	2	Q9AB73 caulobacter
31	156	13.3	643	2	Q9AB73 caulobacter

32	151	12.9	591	2	Q97124 clostridium
33	147.5	12.6	657	2	Q8Y350 ralsconia s
34	147	12.5	660	2	Q8Y350 ralsconia s
35	146.5	12.5	128	2	Q8Y350 ralsconia s
36	145.5	12.4	491	2	Q8Y350 ralsconia s
37	138	11.8	986	2	Q8Y350 ralsconia s
38	135	11.5	513	2	Q8Y350 ralsconia s
39	134	11.4	115	2	Q8Y350 ralsconia s
40	134	11.4	115	2	Q8Y350 ralsconia s
41	133	11.3	622	2	Q8Y350 ralsconia s
42	133	11.3	622	2	Q8Y350 ralsconia s
43	131	11.2	115	2	Q8Y350 ralsconia s
44	129	11.0	115	2	Q8Y350 ralsconia s
45	109.5	9.3	151	2	Q8Y350 ralsconia s

ALIGNMENTS

RESULT 1

ID	Q9FIU1	PRELIMINARY	PRT	248 AA.
AC	Q9FIU1			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Acid phosphatase.			
GN	Name-pho,			
OS	Enterobacter aerogenes (aerobacter aerogenes).			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Enterobacter.			
NC	NCBI_TaxID=548;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=IFO12010;			
RA	Mihara Y., Udagawa T., Matsui H., Amano Y.;			
RL	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AB044338; BAB18917.1; -.			
DR	HSSP; Q9SIA6; 1D2T.			
DR	GO; GO:00030288; C:periplasmic space (sensus Gram-negative Bact. . .; IEA.			
DR	GO; GO:0003993; F:acid phosphatase activity; IEA.			
DR	InterPro; IPR01158; Acid_Ptase_C1a.			
DR	InterPro; IPR008934; AcPase_VanPase.			
DR	InterPro; IPR001011; Bac_AcPaseA.			
DR	InterPro; IPR000326; Pesterase_PA_PTP.			
DR	Pfam; PF01563; PAP2; 1.			
DR	Pfam; PIRSF00897; Acid_Ptase_C1a; 1.			
DR	PRINTS; PR00483; BACPHTASE.			
DR	PRODOM; PD009838; Bac_AcPaseA; 1.			
DR	SMART; SM00014; acidPc; 1.			
DR	PROSITE; PS01157; ACID_PHOSPH_CL_A; 1.			
SO	SEQUENCE 248 AA; 26563 MW; 20EFA2C25EE62D CRC64;			

Query Match 100.0%; Score 1173; DB 2; Length 248;
Best Local Similarity 100.0%; Pred.No. 7.8e-97;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	LVPAQNDAITKPDLYYLKNAQAIISLALPPPEVGSIAFLNDAMTEKGLLNTERTGK 60
DB	21	LVPAQNDAITKPDLYYLKNAQAIISLALPPPEVGSIAFLNDAMTEKGLLNTERTGK 80
QY	61	LAADANLSAGVNAASSAFSGSPITEKDAFQHLKLTNNMEDAGDATTRSAKEXWRIR 120
DB	81	LAADANLSAGVNAASSAFSGSPITEKDAFQHLKLTNNMEDAGDATTRSAKEXWRIR 140
QY	121	PPFAVGVSTCWTTEBQDKLSKNGSYPSGHTSIGWATVLAIEINPQONEILKRGYELGES 180
DB	141	PPFAVGVSTCWTTEBQDKLSKNGSYPSGHTSIGWATVLAIEINPQONEILKRGYELGES 200
QY	181	RVLGTYHMQSDVDAAKIVGSVVAATLTNTNPAFOOOLQKAKDEFKATQK 228
DB	201	RVLGTYHMQSDVDAAKIVGSVVAATLTNTNPAFOOOLQKAKDEFKATQK 248

RESULT 2

```

O991U0      PRELIMINARY;      PRT;      248 AA.
AC O991U0;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Acid phosphatase.
GN Name-pho;
OS Klebsiella planticola (Raoultella planticola).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Raoultella.
OX NCBI_TaxID=575;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO14939;
RA Mihara Y., Utagawa T., Matsui H., Asano Y.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR HSSP; O9S1A6; 1D2T.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR InterPro; IPR01158; Acid_Phase_C1A.
DR InterPro; IPR008934; AcPase_VanPerase.
DR InterPro; IPR001011; Bac_AcPaseA.
DR Pfam; PF01569; PAP2; 1.
DR PIRSF; PIRSF000897; Acid_Phase_C1A; 1.
DR PRINTS; PR00483; BACPHRTASE.
DR ProDom; PD009838; Bac_AcPaseA; 1.
DR SMART; SM00014; acidPpc; 1.
DR PROSITE; PS01157; ACID_PHOSPH_CL_A; 1.
SQ SEQUENCE 248 AA; 26745 MW; 68f65ca2448eb3ef CRC64;

Query Match
Best Local Similarity 96.8%; Score 1136; DB 2; Length 248;
Matches 221; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 LVPAQNDATTPDLYLTKNAQAIIDSLALPPPEVGSIAFLINDQAMYEKRLNTERGK 60
DB 21 LVPAQNDATTPDLYLTKNAQAIIDSLALPPPEVGSIAFLINDQAMYEKRLNTERGK 80
OY 61 LAADANLSAGVANAFSSAFSGSPITEKDAPOHLKLTNMTIEDAGDATSAKEXYR 120
DB 81 LAADANLSAGVANAFSSAFSGSPITEKDAPOHLKLTNMTIEDAGDATSAKEXYR 140
OY 121 PFAFYGVSTCNTTTEODKLSKNGSYSGHTSIGMATLVLAELINPQRONEILKGYELGES 180
DB 141 PFAFYGVSTCNTTTEODKLSKNGSYSGHTSIGMATLVLAELINPQRONEILKGYELGES 200
OY 181 RVICGYHMQSDVDARIVGSAVAVATLTHTNPAFOOQLQKAKDEFKAKOK 228
DB 201 RVICGYHMQSDVDARIVGSAVAVATLTHTNPAFOOQLQKAKDEFKAKOK 248

RESULT 3
O9RLW6      PRELIMINARY;      PRT;      248 AA.
AC O9RLW6;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Phoc protein precursor (EC 3.1.3.2).
GN Name-phoc;
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCUG 225;
RA Passariello C., Berlutti F., Selan L., Thaller M.C., Rossolini G.;

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RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ250377; CAB59725.1; -.
DR HSSP; O9S1A6; 1D2T.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR01158; Acid_Phase_C1A.
DR InterPro; IPR008934; AcPase_VanPerase.
DR InterPro; IPR001011; Bac_AcPaseA.
DR Pfam; PF01569; PAP2; 1.
DR PIRSF; PIRSF000897; Acid_Phase_C1A; 1.
DR PRINTS; PR00483; BACPHRTASE.
DR ProDom; PD009838; Bac_AcPaseA; 1.
DR SMART; SM00014; acidPpc; 1.
DR PROSITE; PS01157; ACID_PHOSPH_CL_A; 1.
FT SIGNAL 1
FT CHAIN 21
SQ SEQUENCE 248 AA; 27110 MW; ED6E9D8663636BDD CRC64;

Query Match
Best Local Similarity 94.5%; Score 1108; DB 2; Length 248;
Matches 215; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

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OY 1 LVPAQNDATTPDLYLTKNAQAIIDSLALPPPEVGSIAFLINDQAMYEKRLNTERGK 60
DB 21 LVPAQNDATTPDLYLTKNAQAIIDSLALPPPEVGSIAFLINDQAMYEKRLNTERGK 80
OY 61 LAADANLSAGVANAFSSAFSGSPITEKDAPOHLKLTNMTIEDAGDATSAKEXYR 120
DB 81 LAADANLSAGVANAFSSAFSGSPITEKDAPOHLKLTNMTIEDAGDATSAKEXYR 140
OY 121 PFAFYGVSTCNTTTEODKLSKNGSYSGHTSIGMATLVLAELINPQRONEILKGYELGES 180
DB 141 PFAFYGVSTCNTTTEODKLSKNGSYSGHTSIGMATLVLAELINPQRONEILKGYELGES 200
OY 181 RVICGYHMQSDVDARIVGSAVAVATLTHTNPAFOOQLQKAKDEFKAKOK 228
DB 201 RVICGYHMQSDVDARIVGSAVAVATLTHTNPAFOOQLQKAKDEFKAKOK 248

RESULT 4
O9S1A6      PRELIMINARY;      PRT;      249 AA.
AC O9S1A6;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Acid phosphatase (EC 3.1.3.2).
GN Name-pho;
OS Escherichia blattae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=563;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JCM1650;
RA MEDLINE=20296667; PubMed=10835340; DOI=10.1093/emboj/19.11.2412;
RA Ishikawa K., Mihara Y., Gondoh K., Suzuki E., Asano Y.;
RT "X-ray structures of a novel acid phosphatase from Escherichia blattae
and its complex with the transition-state analog molybdate.";
RL EMBO J. 19:2412-2423 (2000).
DR EMBL; AB020481; BAA84942.1; -.
DR PDB; 1D2T; X-ray; A=19-249.
DR PDB; 1B01; X-ray; A/B/C=19-249.
DR PDB; 1IW8; X-ray; A/D/E=19-249; B/C/F=--.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR01158; Acid_Phase_C1A.
DR InterPro; IPR008934; AcPase_VanPerase.
DR InterPro; IPR001011; Bac_AcPaseA.

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DR InterPro; IPR000326; Peesterase_PA_PTP.
 DR Pfam; PF01569; PAP2; 1.
 DR PIRSF; PIRSF000897; Acid_Phase_ClaA; 1.
 DR PRINTS; PR00483; BACPHPTASE.
 DR ProDom; PD009838; Bac_AcPaseA; 1.
 DR SMART; SM00014; acidPpc; 1.
 DR PROSITE; PS01157; ACID_PHOSP_CL_A; 1.
 DR HydroLase.
 SQ SEQUENCE 249 AA; 26956 MW; 7ABAE6CB61FC0CA3 CRC64;

Query Match 93.0%; Score 1091; DB 2; Length 249;
 Best Local Similarity 92.1%; Pred. No. 1.8e-89;
 Matches 210; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 LVPAQNDATTKPDLYLLKNAQAIDSLALLPPPEVGSIAFLNDQAMYEKGRLLRTERGK 60
 DB 21 LVATGNDTTTPDLYLLKNSKSHINLALPPPAVGSIAFLNDQAMYEKGRLLRTERGK 80
 QY 61 LAEDANLSAGVANAFASSAFSPITTEKDAPOHLKLTNTMEDADGLATRSKKEKYMIR 120
 DB 81 LAEDANLSAGVANAFASSAFSPITTEKDAPOHLKLTNTMEDADGLATRSKKEKYMIR 140
 QY 121 PPAFGVSTCNTTEBODKLSKNGSYSGHTSIGMATLVLAELNPOREILKRGYELGSR 180
 DB 141 PPAFGVSTCNTTEBODKLSKNGSYSGHTSIGMATLVLAELNPOREILKRGYELGSR 200
 QY 181 RVICGYHQSDVDARIVGSAVAVATLHTNPAFOQLQKAKDEFATOK 228
 DB 201 RVICGYHQSDVDARIVGSAVAVATLHTNPAFOQLQKAKDEFATOK 248

RESULT 5

ID 050542 PRELIMINARY; PRT; 249 AA.

AC 050542; OSE0542; 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Nonspecific phosphatase.
 GN Name=phon.
 OS Shigella flexneri.
 OG Plasmid pMYSH6000.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Shigella.
 OX NCBI_Taxid=623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=YSH6000;
 RX MEDLINE=96345620; PubMed=8755883;
 RA Uchiya K., Tohnoji M., Nikai T., Sugihara H., Sasaki C.;
 RT "Identification and characterization of phon-sf, a gene on the large
 plasmid of Shigella flexneri 2a encoding a nonspecific phosphatase.";
 RL J. Bacteriol. 178:4548-4554(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=YSH6000;
 RA Uchiya K.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; D82966; BA011655.1; -.
 DR HSSP; Q9S1A6; 1D2T.
 DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
 DR GO; GO:0003993; F:acid phosphatase activity; IEA.
 DR InterPro; IPR011158; Acid_Phase_ClaA.
 DR InterPro; IPR00834; AcPase_VanPase.
 DR InterPro; IPR001011; Bac_AcPaseA.
 DR Pfam; PF01569; PAP2; 1.
 DR PIRSF; PIRSF000897; Acid_Phase_ClaA; 1.
 DR PRINTS; PR00483; BACPHPTASE.
 DR ProDom; PD009838; Bac_AcPaseA; 1.
 DR SMART; SM00014; acidPpc; 1.
 DR PROSITE; PS01157; ACID_PHOSP_CL_A; 1.
 KM Plasmid.

SQ SEQUENCE 249 AA; 27177 MW; 58F34CEB034EB070 CRC64;

Query Match. 89.2%; Score 1046; DB 2; Length 249;
 Best Local Similarity 87.2%; Pred. No. 1.9e-85;
 Matches 198; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 2 VPAGNDATTKPDLYLLKNAQAIDSLALLPPPEVGSIAFLNDQAMYEKGRLLRTERGK 61
 DB 22 IPPGNDVTTTKPDLYLLTNDNAIDSLALLPPPGIGSIAFLNDQAMYEKGRLLRTERGK 81
 QY 62 AEDANLSAGVANAFASSAFSPITTEKDAPOHLKLTNTMEDADGLATRSKKEKYMIR 121
 DB 82 AEDANLSAGVANAFASSAFSPITTEKDAPOHLKLTNTMEDADGLATRSKKEKYMIR 141
 QY 122 PAFVGVSTCNTTEBODKLSKNGSYSGHTSIGMATLVLAELNPOREILKRGYELGSR 181
 DB 142 PAFVGVSTCNTTEBODKLSKNGSYSGHTSIGMATLVLAELNPOREILKRGYELGSR 201
 QY 182 VICGYHQSDVDARIVGSAVAVATLHTNPAFOQLQKAKDEFATOK 228
 DB 202 VICGYHQSDVDARIVGSAVAVATLHTNPAFOQLQKAKDEFATOK 248

RESULT 6

ID 099099 PRELIMINARY; PRT; 249 AA.

AC 099099; O7BCK1;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Phon1, periplasmic non specific acid ohosphatase (Phosphatase precursor).
 GN Name=phon1; Synonyms=phon-sf;
 OS Shigella flexneri.
 OG Plasmid virulence plasmid pMR501, and plasmid pCP301.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Shigella.
 OX NCBI_Taxid=623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=M90T;
 RX MEDLINE=20566792; PubMed=1115111;
 RA Buchrieser C., Glaeser P., Rusnock C., Nedjari H., d'Hauteville H.,
 RA Kunst F., Sansonetti P., Parrot C.;
 RT "The virulence plasmid pMR100 and the repertoire of proteins secreted
 by the type III secretion apparatus of Shigella flexneri.";
 RL Mol. Microbiol. 38:760-771(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC PLASMID=virulence plasmid pMR501;
 RX MEDLINE=21189246; PubMed=11297750;
 RX DOI=10.1128/JAI.69.5.3271-3285.2001;
 RA Verkaesman M.M., Goldberg M.B., Rose D.J., Grotbeck B.J., Burland V.,
 RA Blatner F.R.;
 RT "Complete DNA sequence and analysis of the large virulence plasmid of
 Shigella flexneri.";
 RL Infect. Immun. 69:3271-3285(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=301 / Serotype 2a; PLASMID=pCP301;
 RX MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
 RA Jin O., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
 RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
 RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
 RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
 RA Yu J.;
 RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
 through comparison with genomes of Escherichia coli K12 and O157.";
 RL Nucleic Acids Res. 30:4432-4441(2002).
 DR EMBL; AL391753; CAC05839.1; -.
 DR EMBL; AF348706; AK18512.1; -.
 DR EMBL; AF386526; AL172311.1; -.
 DR HSSP; Q9S1A6; 1D2T.

DR GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
 DR GO:0003993; F:acid phosphatase activity; IEA.
 DR InterPro: IPR011158; Acid_Ptase_C1aB.
 DR InterPro: IPR008934; ACPase_VanPerae.
 DR InterPro: IPR010111; Bac_AcPatasea.
 DR InterPro: IPR000326; Pesterase_PA_PTP.
 DR Pfam: PF01569; PAP2_1.
 DR PIRSF: PIRSF000897; Acid_Ptase_C1aA; 1.
 DR PRINTS: PR00483; BACPHPTASE.
 DR Prodom: PD009838; Bac_AcPatasea; 1.
 DR SMART: SM00014; acidPfc; 1.
 DR SMART: SM00014; acidPfc; 1.
 DR PROSITE: PS01157; ACID_PHOSPH_CL_A; 1.
 DR Complete proteome; Plasmid.
 SQ SEQUENCE 249 AA; 27211 MW; 9051C6C1CE21ABA CRC64;

Query Match 88.9%; Score 1043; DB 2; Length 249;
 Best Local Similarity 87.6%; Pred. No. 3.5e-85;
 Matches 188; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 3 PAGNDATTKPDLYLKNQAIDSLALPPPEVGSIAFLNDQMYEKGRLLRTERGKLA 62
 DB 23 PPGNDVTTKPDLYLKNQAIDSLALPPPEVGSIAFLNDQMYEKGRLLRTERGKLA 82
 QY 63 AEDANISAGGVANAFSSAFSGSPITEKDAPOHLKLTNTMEDAGDLATRSKAKYMRIRP 122
 DB 83 AEDANISAGGVANAFSSAFSGSPITEKDAPOHLKLTNTMEDAGDLATRSKAKYMRIRP 142
 QY 123 AFYGVSTCNTBEDKSKNGSYPSGHTSIGMATVLAELINPORQNEILKRGYELGDSR 182
 DB 143 AFYGVSTCNTBEDKSKNGSYPSGHTSIGMATVLAELINPORQNEILKRGYELGDSR 202
 QY 183 ICGYHMQSDVDARIVGSAVATLTNPAFOOQLOKAKDEFKATOK 228
 DB 203 ICGYHMQSDVDARIVGSAVATLTNPAFOOQLOKAKDEFKATOK 248

RESULT 7
 PHOC_PROST STANDARD; PRT; 248 AA.
 ID PHON_PROST
 AC P26975;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Nonspecific acid phosphatase precursor (EC 3.1.3.2) (NSAP).
 GN Name-phoc;
 OS Providencia stuartii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Providencia.
 OX NCBI_TaxID=588;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PV81;
 RA Riccio M.L., Lombardi G., Chiesurin A., Satta G.;
 RL Submitted (FEB-1992) to the EMBL/Genbank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: A phosphate monoester + H(2)O = an alcohol +
 CC phosphate.
 CC -1- SUBCELLULAR LOCATION: Periplasmic.
 CC -1- SIMILARITY: Belongs to the class A bacterial acid phosphatase
 CC family.
 CC -----
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EMBL: X64820; CAA46032.1; -
 DR PIR: S19888; PROCS.
 DR HSP: O951A6; 102T.
 DR InterPro: IPR011158; Acid_Ptase_C1aA.
 DR InterPro: IPR008934; ACPase_VanPerae.

DR InterPro: IPR001011; Bac_AcPatasea.
 DR InterPro: IPR000326; Pesterase_PA_PTP.
 DR Pfam: PF01569; PAP2_1.
 DR PIRSF: PIRSF000897; Acid_Ptase_C1aA; 1.
 DR PRINTS: PR00483; BACPHPTASE.
 DR Prodom: PD009838; Bac_AcPatasea; 1.
 DR SMART: SM00014; acidPfc; 1.
 DR PROSITE: PS01157; ACID_PHOSPH_CL_A; 1.
 DR Hydrolyase; Periplasmic; Signal.
 FT SIGNAL 1
 FT CHAIN 21
 SQ SEQUENCE 248 AA; 27043 MW; 2122A4B95E767CB2 CRC64;

Query Match 88.2%; Score 1035; DB 1; Length 248;
 Best Local Similarity 85.5%; Pred. No. 1.8e-84;
 Matches 194; Conservative 20; Mismatches 13; Indels 0; Gaps 0;

QY 2 VPAGNDATTKPDLYLKNQAIDSLALPPPEVGSIAFLNDQMYEKGRLLRTERGKLA 61
 DB 22 IPPGNDVTTKPDLYLKNQAIDSLALPPPEVGSIAFLNDQMYEKGRLLRTERGKLA 81
 QY 62 AEDANISAGGVANAFSSAFSGSPITEKDAPOHLKLTNTMEDAGDLATRSKAKYMRIRP 121
 DB 82 AAKADLAAGGVANAFSSAFSGSPITEKDAPEIHLKLTNTMEDAGDLATRSKAKYMRIRP 141
 QY 122 AFYGVSTCNTBEDKSKNGSYPSGHTSIGMATVLAELINPORQNEILKRGYELGDSR 181
 DB 142 AFYGVSTCNTBEDKSKNGSYPSGHTSIGMATVLAELINPORQNEILKRGYELGDSR 201
 QY 182 VICGYHMQSDVDARIVGSAVATLTNPAFOOQLOKAKDEFKATOK 228
 DB 202 VICGYHMQSDVDARIVGSAVATLTNPAFOOQLOKAKDEFKATOK 248

RESULT 8
 PHOC_MORMO STANDARD; PRT; 249 AA.
 ID PHOC_MORMO
 AC P28581;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Major phosphate-irrepressible acid phosphatase precursor (EC 3.1.3.2) (HPAP).
 GN Name-phoc;
 OS Morganella morganii (Proteus morganii).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Morganella.
 OX NCBI_TaxID=582;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 21-40.
 RC STRAIN=RS12;
 RA MEDLINE=94362901; PubMed=8081499;
 RA Thaller M.C., Berlucchi F., Schippa S., Lombardi G., Rossojini G.M.;
 RT "Characterization and sequence of phoc, the principal phosphate-
 RT irrepressible acid phosphatase of Morganella morganii.";
 RL Microbiology 140:1341-1350 (1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCIME 10466;
 RX MEDLINE=20336426; PubMed=10877772;
 RX DOI=10.1128/AEM.66.7.2811-2816.2000;
 RA Mhara Y., Utagawa T., Yamada H., Asano Y.;
 RT "Phosphorylation of nucleosides by the mutated acid phosphatase from
 RT Morganella morganii.";
 RL Appl. Environ. Microbiol. 66:2811-2816 (2000).
 CC -1- CATALYTIC ACTIVITY: A phosphate monoester + H(2)O = an alcohol +
 CC phosphate.
 CC -1- SUBUNIT: Homotetramer.
 CC -1- SUBCELLULAR LOCATION: Periplasmic.
 CC -1- MISCELLANEOUS: Has a pH optimum around 6.
 CC -1- SIMILARITY: Belongs to the class A bacterial acid phosphatase
 CC family.
 CC -----

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X64444; CAA45774.1; -
DR EMBL; AB035805; BAA96744.1; -
DR PIR; S19187; S19187.
DR HSSP; Q9S1A6; 1D2T.
DR InterPro; IPR011158; Acid Phase ClsA.
DR InterPro; IPR008934; AcPase VanPase.
DR InterPro; IPR010111; Bac AcPaseA.
DR InterPro; IPR000326; Peptase PA_PTP.
DR Pfam; PF01569; PAP2; 1.
DR PIRSF; PIRSF000897; Acid Phase ClsA; 1.
DR PRINTS; PR00483; BACPHPTASE.
DR PRODOM; PD009838; Bac AcPaseA; 1.
DR SMART; SM00014; acidPpc; 1.
DR PROSITE; PS01157; ACID_PHOSP_CL_A; 1.
DR Direct protein sequencing; Hydrolyase; Periplasmic; Signal.
KW SIGNAL
FT CHAIN 1 20
FT SIGNAL 21 249
SQ SEQUENCE 249 AA; 26998 MW; C43F3698052B6A5C CRC64;
Major phosphate-irrepressible acid
phosphatase.
Query Match 83.8%; Score 983.5; DB 1; Length 249;
Best Local Similarity 82.9%; Pred. No. 7.6e-80;
Matches 189; Conservative 16; Mismatches 22; Indels 1; Gaps 1;
Qy 2 VPAGDATTGKPDLYLTKNAQATDSLALPPPEVGSIAFLNDQAMYEKGRLLNTERGKLAADA 66
Db 22 IPAGDATTGKPDLYLTKNEQALDSLALPPPEVGSIOFLNDQAMYEKGRLLNTERGKQ 81
Qy 62 AADANLISAGVANAFASSAFSPITEKDAPOHLKLTNNMIEDAGDLATRSAREKYMIRP 121
Db 82 AADADDLAAGVATAFSGAFGPIREKOSPELYKLTNNMIEDAGDLATRSAREKYMIRP 141
Qy 122 FAFYGVSTCNTTEQDKLSKNGSPSGHTSIGMATLVLAELNFORNEILKRGVELGSSR 181
Db 142 FAFYGTETCNTMDQKSLSTNGSPSGHTSIGMATLVLAELNFORNEILKRGVELGSSR 201
Qy 182 VICGHWQSDVDNARIIVGSAAVATHTNPAFOOQLKADDEFKAKTOK 228
Db 202 VICGHWQSDVDNARIIVGSAAVATHTNPAFOOQLKADDEFKAKTOK 249
RESULT 9
087188 PRELIMINARY; PRT; 263 AA.
AC 087188;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Acid phosphatase (PACP) precursor.
GN Name=PnOC;
OS Prevotella intermedia.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Prevotellaceae; Prevotella.
OX NCB1_TaxID=28131;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 25611;
RX MEDLINE=20026825; PubMed=10559178;
RA Chen X., Ansat T., Awano S., Iida T., Barik S., Takehana T.;
RT "Isolation, cloning, and expression of an acid phosphatase containing
RT phosphotyrosyl phosphatase activity from Prevotella intermedia.";
RL EMBL; AB017537; BAA33148.1; -
DR HSSP; Q9S1A6; 1D2T.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.

DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR InterPro; IPR011158; Acid Phase ClsA.
DR InterPro; IPR008934; AcPase VanPase.
DR InterPro; IPR010111; Bac AcPaseA.
DR InterPro; IPR000326; Peptase PA_PTP.
DR Pfam; PF01569; PAP2; 1.
DR PIRSF; PIRSF000897; Acid Phase ClsA; 1.
DR PRINTS; PR00483; BACPHPTASE.
DR PRODOM; PD009838; Bac AcPaseA; 1.
DR SMART; SM00014; acidPpc; 1.
DR PROSITE; PS01157; ACID_PHOSP_CL_A; 1.
KW Signal.
FT SIGNAL 1 20
SQ SEQUENCE 263 AA; 29201 MW; 6AD1C4A6470BF313 CRC64;
Potential.
Query Match 65.9%; Score 773; DB 2; Length 263;
Best Local Similarity 65.8%; Pred. No. 6.1e-61;
Matches 146; Conservative 29; Mismatches 47; Indels 0; Gaps 0;
Qy 7 DATKPDLYLTKNAQATDSLALPPPEVGSIAFLNDQAMYEKGRLLNTERGKLAADA 66
Db 29 DATNPDLYLQDQQTSSLELPPPOPSTIOFLYDPAQYQKGMQNTREGDAVADA 88
Qy 67 NLSAGVANAFASSAFSPITEKDAPOHLKLTNNMIEDAGDLATRSAREKYMIRPFAFG 126
Db 89 RVGGDGVNAPSAFSGAFGIRKSTETPEIKLVLMNREDAGDLATRSAREKYMIRPFAFG 148
Qy 127 VSTCNTTEQDKLSKNGSPSGHTSIGMATLVLAELNFORNEILKRGVELGSSR 186
Db 149 EMTCNPEQDQLSTNGSPSGHTSIGMATLVLAELNFORNEILKRGVELGSSR 208
Qy 187 HMOSVDNARIIVGSAAVATHTNPAFOOQLKADDEFKAKTOK 228
Db 209 HMOSVDNARIIVGSAAVATHTNPAFOOQLKADDEFKAKTOK 250
RESULT 10
0990G5 PRELIMINARY; PRT; 246 AA.
AC 0990G5;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Phn2 (Apy), periplasmic phosphatase, apyrase, ATP diphosphohydrolase
DE (Apyrase).
GN Name=phn2 (apy); Synonym=S0004;
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCB1_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M90T;
RX MEDLINE=20566792; PubMed=1115111;
RA Buchrieser C., Glaeser P., Rusnik C., Nedjari H., d'Hauteville H.,
RA Kunst F., Sansonetti P., Parosot C.;
RT "The virulence plasmid pWR100 and the repertoire of proteins secreted
RT by the type III secretion apparatus of Shigella flexneri.";
RL Mol. Microbiol. 38:760-771(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC PLASMID=virulence plasmid pWR501;
RX MEDLINE=21189246; PubMed=11292750;
RX DOI=10.1128/IAI.69.5.3271-3285.2001;
RA Verheesman M.M., Goldberg M.B., Rose D.J., Groetbeck E.J., Burland V.,
RA Blatter F.R.;
RT "Complete DNA sequence and analysis of the large virulence plasmid of
RT Shigella flexneri.";
RL Infect. Immun. 69:3271-3285(2001).
RL EMBL; AL391753; CAC05771.1; -
DR EMBL; AF348706; AAK18315.1; -
DR HSSP; Q9S1A6; 1IWS.

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DR GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR GO:0003993; F:acid phosphatase activity; IEA.
DR GO:0016787; F:hydrolase activity; IEA.
DR InterPro: IPR01158; Acid_Pase_C18A.
DR InterPro: IPR008934; AcPase_VanPase.
DR InterPro: IPR01011; Bac_AcPaseA.
DR InterPro: IPR00326; Pesterase_PA_PTP.
DR Pfam: PF01569; PAP2; 1.
DR PIRSF: PIRSF00897; Acid_Pase_C18A; 1.
DR PRINTS: PR00483; BACPHPTASE.
DR ProDom: PD009838; Bac_AcPaseA; 1.
DR SMART: SM00014; acidPPC; 1.
DR Hydrolase; PfamId.
SQ SEQUENCE 246 AA; 27559 MW; 48D76BD8C7885E5 CRC64;

Query Match 49.4%; Score 579.5; DB 2; Length 246;
Best Local Similarity 50.9%; Pred. No. 1,2e-43;
Matches 113; Conservative 40; Mismatches 64; Indels 5; Gaps 2;

QY 2 VPAGNDATTKPDLYLKNAQALDSLALPPPEVGSIAFLNDQMYEKRLRTERGKL 61
DB 18 IPSANALKAEG--FLTQOTSPLSLIPPEPAEDSVFLADKAHYFGSLRDANKVRL 74
QY 62 AADANLSAGGVANASSAFSPITEKDAPOHLKLTNNIEDAGDIATSAKEKYRIRP 121
DB 75 ASEDAYYENFGL--AFSDAYGMDISRENTPIYLQTLTQVLODSHDYAVNAKEYKVRP 132
QY 122 FAFYGVSTCNTTEBDKLSKNGSPSGHTSIGMATVLAIEINPORONEILKRGYEGER 181
DB 133 FVIYKATCTPDDDEKALITGSYPGSHAFGMAVALILAEINFORKAEILRRGFEGER 192
QY 182 VICGHWQSDVDARIYGSAAVATLHTNPAFOOLOKAKPEF 223
DB 193 VICGHWQSDVEKRLMGASVAVLHNTPEFTKSLSEAKKEF 234

RESULT 11
Q59909 PRELIMINARY; PRT; 246 AA.
AC 059909; Q7BCQ3;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE ATP diphosphohydrolase, apyrase precursor (EC 3.6.1.5) (Apyrase).
GN Name=apy; flexneri.
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxId=623;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2a;
RA Ramchandran V., Sankaran K., Subrahmanyam Y.V.B.K., Ramakrishnan R.,
RA Datta S., Roy R.K.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=2a;
RA Roy R.;
RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=301 / Serotype 2a; PLASMID=PCP301;
RX MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang Y., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157."
RL Nucleic Acids Res. 30:4432-4441(2002).

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DR EMBL: U04539; AAA21206.1; -.
DR EMBL: AF386526; AAL72358.1; -.
DR HSSP: Q931A6; 1IW8.
DR GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR GO:0003993; F:acid phosphatase activity; IEA.
DR GO:0004050; F:apyrase activity; IEA.
DR GO:0016787; F:hydrolase activity; IEA.
DR InterPro: IPR01158; Acid_Pase_C18A.
DR InterPro: IPR008934; AcPase_VanPase.
DR InterPro: IPR01011; Bac_AcPaseA.
DR InterPro: IPR00326; Pesterase_PA_PTP.
DR Pfam: PF01569; PAP2; 1.
DR PIRSF: PIRSF00897; Acid_Pase_C18A; 1.
DR PRINTS: PR00483; BACPHPTASE.
DR ProDom: PD009838; Bac_AcPaseA; 1.
DR SMART: SM00014; acidPPC; 1.
DR Complete proteome; Hydrolase; Signal.
FT SIGNAL 1 23 Potential.
SQ SEQUENCE 246 AA; 27573 MW; B81737D9E6143912 CRC64;

Query Match 49.0%; Score 574.5; DB 2; Length 246;
Best Local Similarity 50.5%; Pred. No. 3.5e-43;
Matches 112; Conservative 40; Mismatches 65; Indels 5; Gaps 2;

QY 2 VPAGNDATTKPDLYLKNAQALDSLALPPPEVGSIAFLNDQMYEKRLRTERGKL 61
DB 18 IPSANALKAEG--FLTQOTSPLSLIPPEPAEDSVFLADKAHYFGSLRDANKVRL 74
QY 62 AADANLSAGGVANASSAFSPITEKDAPOHLKLTNNIEDAGDIATSAKEKYRIRP 121
DB 75 ASEDAYYENFGL--AFSDAYGMDISRENTPIYLQTLTQVLODSHDYAVNAKEYKVRP 132
QY 122 FAFYGVSTCNTTEBDKLSKNGSPSGHTSIGMATVLAIEINPORONEILKRGYEGER 181
DB 133 FVIYKATCTPDDDEKALITGSYPGSHAFGMAVALILAEINFORKAEILRRGFEGER 192
QY 182 VICGHWQSDVDARIYGSAAVATLHTNPAFOOLOKAKPEF 223
DB 193 VICGHWQSDVEKRLMGASVAVLHNTPEFTKSLSEAKKEF 234

RESULT 12
Q931G8 PRELIMINARY; PRT; 246 AA.
AC Q931G8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Apyrase (EC 3.6.1.5).
GN Name=apy;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxId=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HN280;
RX MEDLINE=22167055; PubMed=12177345;
RA Santapaoia D., Casali M., Petrucca A., Presutti C., Zagaglia C.,
RA Berlucchi F., Colonna B., Nicoletti M.;
RT "Enteroinvasive Escherichia coli virulence-plasmid-carried apyrase
RT (apy) and ospB genes are organized as a bicistronic operon and are
RT subject to differential expression."
RL Microbiology 148:2519-2529(2002).
DR EMBL: AJ13184; CAC67470.1; -.
DR HSSP: Q931A6; 1IW8.
DR GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR GO:0003993; F:acid phosphatase activity; IEA.
DR GO:0004050; F:apyrase activity; IEA.
DR GO:0016787; F:hydrolase activity; IEA.
DR InterPro: IPR01158; Acid_Pase_C18A.
DR InterPro: IPR008934; AcPase_VanPase.

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DR InterPro; IPR001011; Bac AcPcaseA.
DR InterPro; IPR000326; Peesterase_PA_PTP.
DR Pfam; PF01569; PAP2; 1.
DR PIRSF; PIRSF000897; Acid_Phase_C1A; 1.
DR PRINTS; PR00483; BACPHPTASE.
DR ProDom; PD009838; Bac AcPcaseA; 1.
DR SMART; SM00014; acidPfc; 1.
KW HydroLase; Plasmid.
SQ SEQUENCE 246 AA; 27574 MW; DAIF901BEB075F4 CRC64;

Query Match 48.9%; Score 573.5; DB 2; Length 246;
Best Local Similarity 50.5%; Pred. No. 4,3e-43;
Matches 112; Conservative 40; Mismatches 65; Indels 5; Gaps 2;

QY 2 VPAGNDATTKPDLYLTKNAQAIDSLALPPPEVGSIAFLNDQAMYEKGRLLRNTERRKL 61
DB 18 IPSANALKAEG---FLTQOTSPDISLILPPPAEDSVVFOADKAHYEFGRLRDANRVRL 74
QY 62 AAEDANLSAGVANAFSSAFSGPITEKDAPOHLKLLTMNIEDAGDLATRSAREKYMRIIP 121
DB 75 ASEDAYYENFGL--AFSDAYGMDISRENTPIYLQLLTVLQDSDHYAVRNAAEYKRYRP 132
QY 122 PAFYGVSTCNTTEODKLSKNGSPSGHTSIGMATLVLAELNPOKONELKRGYELGSR 181
DB 133 FVLYKDATCTPDKDEKMAITGSPSGHASFQWAVALLAEINPQKAEILRGRYEFGRSR 192
QY 182 VICGHWQSDVDAAIRIVGSAVVATLHTNPAFOOQLOKAKDEF 223
DB 193 VICGHWQSDVDAAIRIVGSAVVATLHTNPAFOOQLOKAKDEF 223

RESULT 13

06XW11 PRELIMINARY; PRT; 246 AA.
AC Q6XW11;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE PhosN2.
GN Name=PhosN2;
OS Shigella flexneri.
OC Plasmid pINV P6 M1382.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22935215; PubMed=14573649;
RX DOI=10.1128/IAI.71.11.6298-6306.2003;
RA Ian R., Stevenson G., Reeves P.R.;
RT "Comparison of two major forms of the Shigella virulence plasmid pINV:
RT positive selection is a major force driving the divergence.";
RL Infect. Immun. 71:6298-6306(2003).
DR EMBL; AY206428; AAP78968.1; .
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR InterPro; IPR01158; Acid_Phase_C1A.
DR InterPro; IPR008334; AcPase VanPase.
DR InterPro; IPR001011; Bac AcPcaseA.
DR InterPro; IPR000326; Peesterase_PA_PTP.
DR PIRSF; PIRSF000897; Acid_Phase_C1A; 1.
DR PRINTS; PR00483; BACPHPTASE.
DR ProDom; PD009838; Bac AcPcaseA; 1.
DR SMART; SM00014; acidPfc; 1.
KW Plasmid.
SQ SEQUENCE 246 AA; 27560 MW; DASE971B99B70583 CRC64;

Query Match 48.5%; Score 568.5; DB 2; Length 246;
Best Local Similarity 50.0%; Pred. No. 1.2e-42;
Matches 111; Conservative 40; Mismatches 66; Indels 5; Gaps 2;

QY 2 VPAGNDATTKPDLYLTKNAQAIDSLALPPPEVGSIAFLNDQAMYEKGRLLRNTERRKL 61
DB 18 IPSANALKAEG---FLTQOTSPDISLILPPPAEDSVVFOADKAHYEFGRLRDANRVRL 74

DB 18 IPSANALKAEG---FLTQOTSPDISLILPPPAEDSVVFOADKAHYEFGRLRDANRVRL 74
QY 62 AAEDANLSAGVANAFSSAFSGPITEKDAPOHLKLLTMNIEDAGDLATRSAREKYMRIIP 121
DB 75 ASEDAYYENFGL--AFSDAYGMDISRENTPIYLQLLTVLQDSDHYAVRNAAEYKRYRP 132
QY 122 PAFYGVSTCNTTEODKLSKNGSPSGHTSIGMATLVLAELNPOKONELKRGYELGSR 181
DB 133 FVLYKDATCTPDKDEKMAITGSPSGHASFQWAVALLAEINPQKAEILRGRYEFGRSR 192
QY 182 VICGHWQSDVDAAIRIVGSAVVATLHTNPAFOOQLOKAKDEF 223
DB 193 VICGHWQSDVDAAIRIVGSAVVATLHTNPAFOOQLOKAKDEF 223

RESULT 14

06AKP1 PRELIMINARY; PRT; 280 AA.
AC Q6AKP1;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Probable acid phosphatase.
GN OrderedLocusNames=DP2355;
OS Desulfotalea psychrophila.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacteriales;
OC Desulfobulbaceae; Desulfotalea.
OX NCBI_TaxID=84980;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LSV54 / DSM 12343;
RX PubMed=15305914;
RA Rabus R., Ruepp A., Frickey T., Rattei T., Farmann B., Stark M.,
RA Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,
RA Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
RA Klenk H.-P.;
RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
RT from permanently cold Arctic sediments.";
RL Environ. Microbiol. 6:887-902(2004).
DR EMBL; CR522870; CAG37084.1; .
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR InterPro; IPR01158; Acid_Phase_C1A.
DR InterPro; IPR008334; AcPase VanPase.
DR InterPro; IPR008938; AcPase VanPase.
DR InterPro; IPR001011; Bac AcPcaseA.
DR InterPro; IPR000326; Peesterase_PA_PTP.
DR Pfam; PF01569; PAP2; 1.
DR PIRSF; PIRSF000897; Acid_Phase_C1A; 1.
DR PRINTS; PR00483; BACPHPTASE.
DR ProDom; PD009838; Bac AcPcaseA; 1.
DR SMART; SM00014; acidPfc; 1.
DR PROSITE; PS01157; ACID_PHOSPH_CL_A; 1.
KW Complete proteome.
SQ SEQUENCE 280 AA; 30742 MW; C8231006557991F4 CRC64;

Query Match 42.2%; Score 495.5; DB 2; Length 280;
Best Local Similarity 46.6%; Pred. No. 5e-36;
Matches 103; Conservative 36; Mismatches 77; Indels 5; Gaps 2;

QY 6 NDATTKPDLYLTKNAQAIDSLALPPPEVGSIAFLNDQAMYEKGRLLRNTERRKL 61
DB 26 NDLOPIKLVLDGVIADLTLPDLSALLPQPAKESTFALDREVSXKSLRLDRTARVTL 85
QY 62 AAEDANLSAGVANAFSSAFSGPITEKDAPOHLKLLTMNIEDAGDLATRSAREKYMRIIP 121
DB 86 AARBARLTFPQAAAFSCALGVPISEERTPHLYMLRHTLLTDA--LSTDKAKDNNRRTRP 144
QY 122 PAFYGVSTCNTTEODKLSKNGSPSGHTSIGMATLVLAELNPOKONELKRGYELGSR 181
DB 145 FVNVGEVPTCPQOQBOLKKSISYSGHTSIGMATLVLLIVEVSPQTDAILRGMVFGSR 204
QY 182 VICGHWQSDVDAAIRIVGSAVVATLHTNPAFOOQLOKAKDEF 222

Db 205 IVCNHWQSDVWGRIMGAIVARLHADPAFLAEIEVAKAE 245

RESULT 15

ID PHON_SALTY STANDARD; PRT; 250 AA.

AC P26976;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Nonspecific acid phosphatase precursor (EC 3.1.3.2) (NSAP).

GN Name=phon; OrderedLocustNames=Stm4319;

OS Salmonella typhimurium.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Salmonella.

OX NCBI_TaxID=602;

RM [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 14028 / SGSG 2980;

RX MEDLINE=92224869; PubMed=1339343;

RA Grolman E.A., Saier M.H., Jr., Ochman H.,

RT "Horizontal transfer of a phosphatase gene as evidence for mosaic

RT structure of the Salmonella genome.";

RL EMBO J. 11:1309-1316(1992).

RM [2]

RP SEQUENCE FROM N.A.

RC STRAIN=LT2;

RX MEDLINE=92041557; PubMed=1938882;

RA Kasehara M., Nakata A., Shinagawa H.,

RT "Molecular analysis of the Salmonella typhimurium phon gene, which

RT encodes nonspecific acid phosphatase.";

RL J. Bacteriol. 173:6760-6765(1991).

RM [3]

RP SEQUENCE FROM N.A.

RC STRAIN=LT7 / SGSC1412 / ATCC 700720;

RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;

RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,

RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,

RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,

RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,

RA Waterston R., Wilson R.K.;

RT "Complete genome sequence of Salmonella enterica serovar Typhimurium

RT LT2.";

RL Nature 413:852-856(2001).

CC -1- CATALYTIC ACTIVITY: A phosphate monoester + H(2)O = an alcohol +

CC phosphate.

CC -1- SUBUNIT: Homodimer (Probable).

CC -1- SUBCELLULAR LOCATION: Periplasmic.

CC -1- SIMILARITY: Belongs to the class A bacterial acid phosphatase

CC family.

CC -1- CAUTION: Ref.2 sequence differs from that shown in the C-terminus

CC due to a frameshift.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

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CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; X63599; CAA45144.1; -;

DR EMBL; X59036; CAA41760.1; ALT_FRAME.

DR EMBL; AE008902; AAL23143.1; -;

DR PIR; S20958; A41330.

DR HSP; Q9S1A6; I1W8.

DR StyGene; SG10292; phon.

DR InterPro; IPR01158; Acid_Phase_C1SA.

DR InterPro; IPR008934; AcPase_Vanperase.

DR InterPro; IPR001011; Bac_AcPaseA.

DR InterPro; IPR000326; Pesterase_PA_PTP.

DR Pfam; PF01569; PAP2; 1.

DR PIRSF; PIRSF00897; Acid_Phase_C1SA; 1.

DR PRINTS; PR00483; BACPHPTASE.

DR PRODom; PD009338; Bac AcPaseA; 1.

DR SMART; SM00014; acidPc; 1.

DR PROSITE; PS01157; ACID_PHOSP_CL_A; 1.

KT Complete proteome; Hydrolase; periplasmic; Signal.

FT SIGNAL 21 20 potential.

FT CHAIN 21 250 Nonspecific acid phosphatase.

SQ SEQUENCE 250 AA; 28382 MW; CPE8DA40B5D5753 CRC64;

Query Match 41.2%; Score 483; DB 1; Length 250;

Best Local Similarity 47.0%; Pred. No. 5,7e-35;

Matches 95; Conservative 33; Mismatches 74; Indels 0; Gaps 0;

Qy 21 QAIISLLLPPEPVGSIAPNDQMYEKRLNTERGKLAEDANLSAGVANAESSA 80

Db 31 ESVNSQYLLPPPPNDPPAIRYDKEAYFKGYAIGSRWQAAEDADVSENIARISPV 90

Qy 81 FGSPTKEKAPQLHKLJTNMIEDAGDLATRSAREKYNRIRPFAYGVSTCNTTEQDKLSK 140

Db 91 VGAKINPKDPEETWNMLKNLLTWGYYATASAKKYVTRTPFVLFNHSSTCRPEDENTLRK 150

Qy 141 NGSPSGHTSIGMTALVLAIEINQRONEILKRGVEIGESRVTCGYTQSDVDAARIYGS 200

Db 151 NGSPSGHTYVGLTALVLSERPERAQLARRGMEGQSRVTCGAHWQSDVDAGRYVGA 210

Qy 201 AVVATLHTNPAPFOOQLOKADDE 222

Db 211 VEPARLOTIRAFQSLAKVREE 232

Search completed: March 2, 2005, 20:26:49

Job time : 114.255 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 2, 2005, 20:26:57 ; Search time 86.4314 Seconds
(without alignments)
865.359 Million cell updates/sec

Title: US-09-807-990A-125

Perfect score: 1173

Sequence: 1 LVPAQNDATKPDLYYLKNA.....NDPAQQQLQKAKDEFAKTQK 228

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1385339 seqs, 328044528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
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12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1173	100.0	248	9	US-09-727-578-24 Sequence 24, Appl
2	1136	96.8	248	9	US-09-727-578-26 Sequence 26, Appl
3	1091	93.0	231	9	US-09-727-578-8 Sequence 8, Appl
4	1091	93.0	249	9	US-09-727-578-7 Sequence 7, Appl
5	1035	88.2	248	9	US-09-727-578-22 Sequence 22, Appl
6	983.5	83.8	229	9	US-09-727-578-4 Sequence 4, Appl
7	983.5	83.8	249	9	US-09-727-578-3 Sequence 3, Appl
8	983.5	83.8	249	16	US-10-220-481-116 Sequence 116, App
9	772	65.8	244	9	US-09-727-578-28 Sequence 28, Appl
10	133	11.3	622	9	US-09-738-626-4817 Sequence 4817, Ap
11	105	9.0	414	16	US-10-437-963-165801 Sequence 165801,
12	97	8.3	20	9	US-09-727-578-1 Sequence 1, Appl
13	96.5	8.2	647	16	US-10-437-963-112291 Sequence 112291,

14	96	8.2	178	15	US-10-282-122A-77490 Sequence 77490, A
15	93.5	8.0	528	15	US-10-424-599-210277 Sequence 210277,
16	93.5	8.0	611	15	US-10-424-599-210275 Sequence 210275,
17	93.5	8.0	611	15	US-10-425-114-49161 Sequence 49161, A
18	92	7.8	159	9	US-09-738-626-6679 Sequence 6679, App
19	92	7.8	159	15	US-10-627-476-102 Sequence 102, App
20	92	7.8	408	15	US-10-369-493-9754 Sequence 9754, App
21	90.5	7.7	921	14	US-10-281-866-2 Sequence 2, Appl
22	90	7.7	201	14	US-10-156-761-7677 Sequence 7677, Ap
23	90	7.7	437	15	US-10-282-122A-66585 Sequence 66585, A
24	90	7.7	1610	15	US-10-369-493-3448 Sequence 3448, Ap
25	89	7.6	608	15	US-10-369-493-5228 Sequence 5228, Ap
26	88.5	7.5	168	9	US-09-738-626-6676 Sequence 6676, Ap
27	88.5	7.5	1707	14	US-10-223-070-13 Sequence 13, Appl
28	88	7.5	265	15	US-10-424-599-243256 Sequence 243256,
29	87.5	7.5	1127	16	US-10-437-963-140467 Sequence 140467,
30	86.5	7.4	221	15	US-10-282-122A-69103 Sequence 69103, A
31	86	7.3	803	16	US-10-437-963-132702 Sequence 132702,
32	85	7.2	305	15	US-10-369-493-1179 Sequence 1179, Ap
33	85	7.2	766	14	US-10-317-832-120 Sequence 120, App
34	84.5	7.2	326	15	US-10-282-122A-56065 Sequence 56065, A
35	84	7.1	1040	16	US-10-437-963-140470 Sequence 140470,
36	83	7.1	253	15	US-10-282-122A-77898 Sequence 77898, A
37	82.5	7.0	272	15	US-10-282-122A-77471 Sequence 77471, A
38	82.5	7.0	638	16	US-10-437-963-185382 Sequence 185382,
39	82	7.0	218	15	US-10-415-554-2 Sequence 2, Appl
40	82	7.0	239	16	US-10-767-701-39668 Sequence 39668, A
41	82	7.0	447	15	US-10-335-977-9671 Sequence 9671, Ap
42	81.5	6.9	198	15	US-10-282-122A-50258 Sequence 50258, A
43	81.5	6.9	260	16	US-10-408-765A-1756 Sequence 1756, Ap
44	81.5	6.9	307	16	US-10-767-701-41868 Sequence 41868, A
45	81.5	6.9	320	16	US-10-437-963-201944 Sequence 201944,

ALIGNMENTS

RESULT 1

US-09-727-578-24

Sequence 24, Application US/09727578

GENERAL INFORMATION:

Publication No. US20020004590A1

APPLICANT: MIHARA, YASUHIRO

APPLICANT: UTAHARA, TAKASHI

APPLICANT: YAMADA, HIDEAKI

APPLICANT: ASANO, YASUHIRO

TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE

TITLE OF INVENTION: ESTER

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09727, 578

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/975, 698

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 0010-0885-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Enterobacter aerogenes
STRAIN: IFO 12010
US-09-727-578-24

Query Match 100.0%; Score 1173; DB 9; Length 248;
Best Local Similarity 100.0%; Pred. No. 3e-113;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVPAQNDATTKPDLYLYKNAQAIDSLALPPPEVGSIAFLNDQAMYEKRLRNTERGK 60
DB 21 LVPAQNDATTKPDLYLYKNAQAIDSLALPPPEVGSIAFLNDQAMYEKRLRNTERGK 80
QY 61 LAEDANLSAGVANAFSAFSGPITEKAPQLHKLITNMIEDAGDLATRSAREKYMIR 120
DB 81 LAEDANLSAGVANAFSAFSGPITEKAPQLHKLITNMIEDAGDLATRSAREKYMIR 140
QY 121 PFAFYGVSTCNTTEBODKLSKNGSYPSGHTSIGMATLVLAELNFORONEILKRGYELGES 180
DB 141 PFAFYGVSTCNTTEBODKLSKNGSYPSGHTSIGMATLVLAELNFORONEILKRGYELGES 200
QY 181 RVICGYHWSQVDVDAARIYGSANVATLHTNPAFOOOLQKADFEAKTOK 228
DB 201 RVICGYHWSQVDVDAARIYGSANVATLHTNPAFOOOLQKADFEAKTOK 248

RESULT 2

US-09-727-578-26
Sequence 26, Application US/09727578
Publication No. US20020004590A1

GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
TITLE OF INVENTION: ESTER
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/727,578
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Klebsiella planticola
STRAIN: IFO 14939
US-09-727-578-26

Query Match 96.8%; Score 1136; DB 9; Length 248;
Best Local Similarity 96.9%; Pred. No. 2.1e-109;
Matches 221; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 LVPAQNDATTKPDLYLYKNAQAIDSLALPPPEVGSIAFLNDQAMYEKRLRNTERGK 60
DB 21 LVPAQNDATTKPDLYLYKNAQAIDSLALPPPEVGSIAFLNDQAMYEKRLRNTERGK 80
QY 61 LAEDANLSAGVANAFSAFSGPITEKAPQLHKLITNMIEDAGDLATRSAREKYMIR 120
DB 81 LAEDANLSAGVANAFSAFSGPITEKAPQLHKLITNMIEDAGDLATRSAREKYMIR 140
QY 121 PFAFYGVSTCNTTEBODKLSKNGSYPSGHTSIGMATLVLAELNFORONEILKRGYELGES 180
DB 141 PFAFYGVSTCNTTEBODKLSKNGSYPSGHTSIGMATLVLAELNFORONEILKRGYELGES 200
QY 181 RVICGYHWSQVDVDAARIYGSANVATLHTNPAFOOOLQKADFEAKTOK 228
DB 201 RVICGYHWSQVDVDAARIYGSANVATLHTNPAFOOOLQKADFEAKTOK 248

RESULT 3

US-09-727-578-8
Sequence 8, Application US/09727578
Publication No. US20020004590A1

GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
TITLE OF INVENTION: ESTER
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/727,578
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Escherichia blattae
STRAIN: JCM 1650
US-09-727-578-8

Query Match 93.0%; Score 1091; DB 9; Length 231;
Best Local Similarity 92.1%; Pred. No. 9 1e-105; Indels 0; Gaps 0;
Matches 210; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 LVPAAGNDATKPDLYLLKNAQAIDSLALLPPPEVGSIAFLINDQAMYEKGLRLNTERGK 60
DB 3 LVATGNDTTRKPDLYLLKNSAINSALLPPPAVGSIAFLINDQAMEGRLRLNTERGK 62
QY 61 LAEADANLSAGVANAFAFGSPITTEKDAPOHLKLTNMIEDAGDLATRSAXEYMRIR 120
DB 63 LAEADANLSGGVANAFAFGSPITTEKDAPOHLKLTNMIEDAGDLATRSAXEYMRIR 122
QY 121 PPAFGVSTCNTTEODKLSKSGSPSGHTSIGMATLVLAELNFORONEILKRGYEIGES 180
DB 123 PPAFGVSTCNTTEODKLSKSGSPSGHTSIGMATLVLAELNFORONEILKRGYEIGES 182
QY 181 RVICGYHMQSDVDAARIYGSAAVVAITLHTNPAFOOQLOKAKDEFAPKTOK 228
DB 183 RVICGYHMQSDVDAARIYGSAAVVAITLHTNPAFOOQLOKAKDEFAPKTOK 230

RESULT 4
US-09-727-578-7
Sequence 7, Application US/09727578
Publication No. US20020004590A1
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: YAMADA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIRO
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/727,578
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:

ORGANISM: Escherichia blattae
STRAIN: JCM 1650
US-09-727-578-7

Query Match 93.0%; Score 1091; DB 9; Length 249;
Best Local Similarity 92.1%; Pred. No. 1e-104; Indels 0; Gaps 0;
Matches 210; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 LVPAAGNDATKPDLYLLKNAQAIDSLALLPPPEVGSIAFLINDQAMYEKGLRLNTERGK 60
DB 21 LVATGNDTTRKPDLYLLKNSAINSALLPPPAVGSIAFLINDQAMEGRLRLNTERGK 80
QY 61 LAEADANLSAGVANAFAFGSPITTEKDAPOHLKLTNMIEDAGDLATRSAXEYMRIR 120
DB 81 LAEADANLSGGVANAFAFGSPITTEKDAPOHLKLTNMIEDAGDLATRSAXEYMRIR 140
QY 121 PPAFGVSTCNTTEODKLSKSGSPSGHTSIGMATLVLAELNFORONEILKRGYEIGES 180
DB 141 PPAFGVSTCNTTEODKLSKSGSPSGHTSIGMATLVLAELNFORONEILKRGYEIGES 200
QY 181 RVICGYHMQSDVDAARIYGSAAVVAITLHTNPAFOOQLOKAKDEFAPKTOK 228
DB 201 RVICGYHMQSDVDAARIYGSAAVVAITLHTNPAFOOQLOKAKDEFAPKTOK 248

RESULT 5
US-09-727-578-22
Sequence 22, Application US/09727578
Publication No. US20020004590A1
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: YAMADA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIRO
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/727,578
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE: Providencia stuartii
STRAIN: ATCC 29851
US-09-727-578-22

Query Match	88.2%;	Score 1035;	DB 9;	Length 248;
Best Local Similarity	85.5%;	Pred. No. 6.7e-99;		
Matches 194;	Conservative 20;	Mismatches 13;	Indels	

Qy	2	VPGNNDTTPDLYLXKMOAIDSLALPPPEVSI	FLNDQAMYEGRLLRNTBEGKL	61
Db	22	IPGNDVTTKPDLYLKNSOALDSLALPPPEVSI	FLNDQAMYEGRLLRNTBEGQ	81
Qy	62	AAEDANISAGVANAESSAFSEITEKAPOLHKL	TNMIEDAGLATRSAXEYMRIRP	121
Db	82	AAADADLAAGVANAESEAFGYITEKAPPEIHL	KLTNMIEDAGLATRSAXEYMRIRP	141
Qy	122	FARYGSTCTTTEODKLSTKSGSYPSGHS	IGWATLVLAELNFORONEILRGYELGSR	181
Db	142	FARYGAATCTTKODKLSTKSGSYPSGHT	IGWASALVSEINPENODKILRGYELGSR	201
Qy	182	VICGYMOSDVAARIVSGAVAVATLHTNPA	FOOQIOXKXDEFAKTQK	228
Db	202	VICGYMOSDVAARIVASGAVATLHSHNE	FOKQIOXKXDEFAKTQK	248

RESULT 6

```

1  ? Sequence 4, Application US/09727578
2  ? Publication No. US20020004590A1
3  ? GENERAL INFORMATION:
4  ? APPLICANT: MIHARA, YASUHIRO
5  ? APPLICANT: UTAGAMA, TAKASHI
6  ? APPLICANT: YAMADA, HIDEAKI
7  ? APPLICANT: ASANO, YASUHIKA
8  ? TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
9  ? TITLE OF INVENTION: ESTER
10 ? NUMBER OF SEQUENCES: 30
11 ? CORRESPONDENCE ADDRESS:
12 ? ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
13 ? STREET: 1155 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
14 ? CITY: ARLINGTON
15 ? STATE: VIRGINIA
16 ? COUNTRY: USA
17 ? ZIP: 22202
18 ? COMPUTER READABLE FORM:
19 ? MEDIUM TYPE: Floppy disk
20 ? COMPUTER: IBM PC compatible
21 ? OPERATING SYSTEM: PC-DOS/MS-DOS
22 ? SOFTWARE: PatentIn Release #1.0, Version #1.30
23 ? CURRENT APPLICATION DATA:
24 ? APPLICATION NUMBER: US/09/727,578
25 ? FILING DATE:
26 ? CLASSIFICATION:
27 ? PRIOR APPLICATION DATA:
28 ? APPLICATION NUMBER: 08/975,698
29 ? FILING DATE:
30 ? ATTORNEY/AGENT INFORMATION:
31 ? NAME: OBLON, NORMAN F.
32 ? REGISTRATION NUMBER: 24,618
33 ? REFERENCE/DOCKET NUMBER: 0010-0885-0
34 ? TELECOMMUNICATION INFORMATION:
35 ? TELEPHONE: (703) 413-3000
36 ? TELEFAX: (703) 413-2220
37 ? INFORMATION FOR SEQ ID NO: 4:
38 ? SEQUENCE CHARACTERISTICS:
39 ? LENGTH: 229 amino acids
40 ? TYPE: amino acid
41 ? TOPOLOGY: linear
42 ? MOLECULE TYPE: protein
43 ? ORIGINAL SOURCE:
44 ? ORGANISM: Morganella morganii
45 ? STRAIN: NCIMB 10466
46 ? IS-09-727-578-4

```

Query Match	83.8%;	Score 983.5;	DB 9;	Length 229;
Best Local Similarity	82.9%;	Pred. No. 1.3e-93;		

Matches 189; Conservative 16; Mismatches 22; Indels 1; Gaps 1;

QY 2 VPGAGNATTEPDLXYXKNAQIDSLALPPPEVGSIFLNDQAMYEKGRLLRNTTEGKL 61
Db 2 IPRAGNATTEKPDLYIAKMGQIDSLKLPPPEVGSIOFLNDQAMYEKGRLLRNTTERGKQ 61
QY 62 AAEDANILSAGVYANNAESSAFSPITEKCAPOLHKLNTNIEDAGDILTRSAKEYMRIRP 121
Db 62 AQADADLAAGVAVATAFSGAFGPITEXDSPELYKLNTNIEDAGDILTRSAKEYMYMRIRP 121
QY 122 FARYGVSTCNTTBODKLSKNGSYBEGGHSIGWATLVLAETINFORONEILKRGYEIGESR 181
Db 122 FARYGVSTCNTKQDKLSTNGSYBEGGHSIGWATLVLAETINPANODAILERGYQLGQSR 181
QY 182 VICGYHOSDVDAARIVGSAVAVATLHTNPAFOQLQAKKDEFA-KTQK 228
Db 182 VICGYHOSDVDAARIVGSAVAVATLHTSPADFOQLAKKDEFAKQSK 229

RESULT 7
IIS-09-73

Sequence 3, Application US/09727578
Publication No. US2002004590A1
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTRAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
TITLE OF INVENTION: ESTER
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P. C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/727,578
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Morganella morganii
STRAIN: NCIMB 10466
US-09-727-578-3

```

Query Match      83.8%  Score 983.5; DB: 9; Length 249;
Best Local Similarity  82.9%  Pred. No. 1.5e-93;
Matches 189; Conservative 16; Mismatches 22; Indels 1; Gaps 1;
Ox      2  VPAGNDATTTEDLYYLKNAQAIDSLALPPPEVGSIAFLNDQAMYEKRLRTEREKL 61

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QY 2 VPAGNDATTKPDLYLLKNAQAIDSLALLPPPEVGSI AFLNDQAMY EKGRLLRNTERGKL 61

RESULT 9
US-09-727-578-28
Sequence 28, Application US/09727578
Publication No. US20020004590A1
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIKA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
TITLE OF INVENTION: ESTER
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLOH, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P. C.

RESULT 10
US-09-738-626-4817
Sequence 4817, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAMA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125

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Query Match	11.3%;	Score 133;	DB 9;	Length 622;
Best Local Similarity	26.6%;	Pred. No. 0.00014;		
Matches 41;	Conservative 23;	Mismatches 60;	Indels 30;	Gaps 4

QY 99 NMLIEDGDL-----ATRSKXKCYMRIRPPAF-----YGST---C 130
Db 173 NMAETGEGLSGTVDLIEAIRQHAARISNNAKATYYQPRPYRKTETESTEPBAMGEGVDMEYA 222
QY 131 NTTEOD--KLKSNKSGPSGHTSIGMAITVLAINEPQONELIKRGVHELGESRYTCYHW 188
Db 233 NPLRKESBAADGCFPSGHTISAGMATNGLAVAFPOOYDKLMTAAETIGESRIQMGHS 292
QY 189 QSDVDARIVGSAAVATHTHPAFOOLOKADE 222
Db 293 PLDVGIGRVLSTAITAGALNDPNLDSVAKAEFDD 326

```

RESULT 11
US-10-437-963-165801
: Sequence 165801, Application US/10437963
: Publication No. US20040123343A1
: GENERAL INFORMATION:
: APPLICANT: La Rosa, Thomas J.
: APPLICANT: Kovalic, David K.
: APPLICANT: Zhou, Yihua
: APPLICANT: Cao, Yongwei
: APPLICANT: Wu, Wei
: APPLICANT: Boukharov, Andrey A.
: APPLICANT: Barbazuk, Brad
: APPLICANT: Li, Ping
: TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
: TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
: FILE REFERENCE: 38-21(53221)B
: CURRENT APPLICATION NUMBER: US/10/437,963
: CURRENT FILING DATE: 2003-05-14
: NUMBER OF SEQ ID NOS: 204966
: SEQ ID NO 165801
: LENGTH: 414
: TYPE: PRT
: ORGANISM: Oryza sativa
: FEATURE:
: OTHER INFORMATION: Clone ID: PAT_MRT4530_64572C.1.pep
: US-10-437-963-165801

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Query Match	9.0%;	Score 105;	DB 16;	Length 414;
Best Local Similarity	28.8%;	Pred. No. 0.062;		
Matches	45;	Conservative	22;	Mismatches 59; Indels 30; Gaps 7;
QY	22	AIDSLALTPPEPEVGSIAFLNDQAMYEKGRLLRTERG-KLAEDPNLSAGVANA----	76	
	: : :	: : :	: : :	: : :
Db	84	AKHKAHALAPPEPPSKSKSKKNSNSWTW----	PNSRKGGKKAQOPNALAGSAGANGRL	139
	: : :	: : :	: : :	: : :
QY	77	---FSAGFSGSPIT-----EKDAPQLHLKLITNM-----	IEDAGDLATRSASEKXYMARI	119
	: : :	: : :	: : :	: : :
Db	140	PKPFSGDDELVTLPAPRFAERNDAPDLPTLLSRVFKSKQKVEVDRLTAAGSTGKRYMV		199
	: : :	: : :	: : :	: : :
QY	120	REPAFYGVSTCNTTTEQDKLSKNGSKVPSGHSIGMAT		155
	: : :	: : :	: : :	: : :

Db 200 R--ATRGVAGAWYFEVKVLHGS--TGHTRLGWAT 231

RESULT 12
 US-09-727-578-1
 ; Sequence 1, Application US/09727578
 ; Publication No. US2002004590A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MIHARA, YASUHIRO
 ; APPLICANT: UTAGAWA, TAKASHI
 ; APPLICANT: YAMADA, HIDEAKI
 ; APPLICANT: ASANO, YASUHIKA
 ; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
 ; TITLE OF INVENTION: ESTER
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, WAITER & NEUSTADT, P. C.
 ; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
 ; CITY: ARLINGTON
 ; STATE: VIRGINIA
 ; COUNTRY: USA
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/727,578
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/975,698
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: OBLON, NORMAN F
 ; REGISTRATION NUMBER: 24,618
 ; REFERENCE/DOCKET NUMBER: 0010-0885-0
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 413-3000
 ; TELEFAX: (703) 413-2220
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 20 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FRAGMENT TYPE: N-terminal
 ; ORIGINAL SOURCE:
 ; ORGANISM: Morganella morganii
 ; STRAIN: NCIMB 10466
 ; US-09-727-578-1

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Query Match      8.3%: Score 97; DB 9%: Length 20;
Best Local Similarity 94.4%: Pred. No. 0.0055;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CY      2 VPAGNDATTKPDLYYLKN 19
      : ||||| ||||| |||||
Db      2 IPAGNDATTKPDLYYLKN 19

RESULT 13
US-10-437-963-112291
; Sequence 112291, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei

```


RESULT 14

US-10-282-122A-77490

Sequence 77490, Application US/10282122A

Publication No. US2004002912941

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu

APPLICANT: Zamudio, Carlos

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Karl

APPLICANT: Zyekind, Judith

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John

APPLICANT: Carr, Grant

APPLICANT: Yamamoto, Robert

APPLICANT: Forsyth, R.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: EILTRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21 (53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 210277

LENGTH: 528

TYPE: PRT

ORGANISM: Glycine max

FEATURE:

NAME/KEY: unsure

LOCATION: (1)..(528)

OTHER INFORMATION: unsure at all Xaa locations

FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_31908C.1.pep

US-10-424-599-210277

Query Match 8.0%; Score 93.5; DB 15; Length 528; Best Local Similarity 27.5%; Pred. No. 1.4; Matches 50; Conservative 20; Mismatches 73; Indels 39; Gaps 9;

QY 44 QAMYEGRLLRNTERGKTLAEDANLSAGYVNAFFSSAFG---SPITEKD-APQLHLKLTN 99

DB 165 QVAEAKGR-ETETARGVGAGNEGCARTTAYITCTLEKGGTQKPIRBEERSESSRSAME 223

QY 100 MIEDAGDLATRSAXEKYMRIRPFAFYGVSTCTTTEODKLSKNGSYPSGHTSIGMATVLYL 159

DB 224 QISNYSQATQGVKEKYERAKQNA---SETLNTTTQTAQES-----AQAKUL 268

QY 160 AELNPGQREILKRGIELGESRVIICGYHMOSDVDAARIYGSANVATLHTPPAQOOLQKA 219

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RESULT 15
US-10-424-599-210277
: Sequence 210277, Application US/10424599
: Publication No. US20040031072A1
: GENERAL INFORMATION:
: APPLICANT: La Rosa Thomas J
: APPLICANT: Kovalic David K
: APPLICANT: Zhou Yihua
: APPLICANT: Cao Yongwei
: TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
: TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
: FILE REFERENCE: 38-21(53223)B
: CURRENT APPLICATION NUMBER: US/10/424,599
: CURRENT FILING DATE: 2003-04-28
: NUMBER OF SEQ. ID NOS: 285684
: SEQ ID NO 210277
: LENGTH: 528
: TYPE: PRT
: ORGANISM: Glycine max
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (1)..(528)
: OTHER INFORMATION: unsure at all Xaa locations
: FEATURE:
: OTHER INFORMATION: Clone ID: PAT_MRT3847_31908C.1.pep
US-10-424-599-210277

Query Match      8.0%; Score 93.5; DB 15; Length 528;
Best Local Similarity 27.5%; Pred. No.1,4;
Matches 50; Conservative 20; Mismatches 73; Indels 39; Gaps 9;

QY 44 QANVEGRLLRNTERGTLAEDANLSAGVANAFFSSAFG---SPITEKD-APOLHKLTVN 99
      |||||
DB 165 QVVAEKGR-ETETARGRVGHENEGARTTAVITCTLEKGGTQCPRIIBEERSESESSAME 223
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QY 100 MIEDAGDLATRSAXEKYMRIRPFAFYGVSTCTTEBDKLSKNGSSPYSGHTSIGMATALVL 159
      |||||
DB 224 QISNYSQATQGVKEKYERAKQAA---SETLNTTTQDAQES-----AQAKVL 268
      |||||

QY 160 AELNPRQNEILKRGYELGESRVICGYHWOSDVDAARIYGSANVATLHTTPAQQOOLQKA 219
      |||||

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Db	269	A---	AQAKD	ATLEK	GQO-----	GYAVTKDT---	ISSAKTASEKTAPV----	AEKA	309
Qy	220	KD	221						
Db	310	KD	311						

Search completed: March 2, 2005, 20:44:03
Job time : 87.4314 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2005, 20:16:41 ; Search time 29.8039 Seconds
(without alignments)
571.065 Million cell updates/sec

Title: US-09-807-990a-125
Perfect score: 1173
Sequence: 1 LVPAQNDAKTRPDLYLKNA.....NPAFQQLQKAKDEPAKTQK 228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues
Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
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4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/6C_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1173	100.0	248	3	US-08-750-145A-20
2	1173	100.0	248	3	US-08-975-698A-24
3	1173	100.0	248	3	US-09-417-090-24
4	1173	100.0	248	3	US-09-727-578-24
5	1139	97.1	253	4	US-09-489-039A-7933
6	1136	96.8	248	3	US-08-750-145A-22
7	1136	96.8	248	3	US-08-975-698A-26
8	1136	96.8	248	3	US-09-417-090-26
9	1136	96.8	248	3	US-09-727-578-26
10	1091	93.0	231	3	US-08-750-145A-11
11	1091	93.0	231	3	US-08-975-698A-8
12	1091	93.0	231	3	US-09-417-090-8
13	1091	93.0	231	3	US-09-727-578-8
14	1091	93.0	249	3	US-08-750-145A-10
15	1091	93.0	249	3	US-08-975-698A-7
16	1091	93.0	249	3	US-09-417-090-7
17	1091	93.0	249	3	US-09-727-578-7
18	1035	88.2	248	3	US-08-750-145A-18
19	1035	88.2	248	3	US-08-975-698A-22
20	1035	88.2	248	3	US-09-417-090-22
21	1035	88.2	248	3	US-09-727-578-22
22	983.5	83.8	229	3	US-08-750-145A-4
23	983.5	83.8	229	3	US-08-975-698A-4
24	983.5	83.8	229	3	US-09-417-090-4
25	983.5	83.8	229	3	US-09-727-578-4
26	983.5	83.8	249	3	US-08-750-145A-3
27	983.5	83.8	249	3	US-08-975-698A-3

28	983.5	83.8	249	3	US-09-417-090-3	Sequence 3, Appli
29	983.5	83.8	249	3	US-09-727-578-3	Sequence 3, Appli
30	772	65.8	244	3	US-08-750-145A-24	Sequence 24, Appli
31	772	65.8	244	3	US-08-975-698A-28	Sequence 28, Appli
32	772	65.8	244	3	US-09-417-090-28	Sequence 28, Appli
33	772	65.8	244	3	US-09-727-578-28	Sequence 28, Appli
34	317	27.0	252	1	US-07-717-332D-2	Sequence 2, Appli
35	193.5	16.5	943	4	US-09-540-236-3458	Sequence 3458, Ap
36	191.5	16.3	428	4	US-09-489-039A-10941	Sequence 10941, A
37	166	14.2	253	4	US-09-252-991A-28557	Sequence 28557, A
38	153	13.0	987	4	US-09-543-681A-7785	Sequence 7785, Ap
39	97	8.3	20	3	US-08-750-145A-1	Sequence 1, Appli
40	97	8.3	20	3	US-08-975-698A-1	Sequence 1, Appli
41	97	8.3	20	3	US-09-417-090-1	Sequence 1, Appli
42	97	8.3	20	3	US-09-727-578-1	Sequence 1, Appli
43	92.5	7.9	187	4	US-09-328-352-7918	Sequence 7918, Ap
44	92	7.8	159	4	US-09-602-787A-102	Sequence 102, App
45	90.5	7.7	244	4	US-09-543-681A-4595	Sequence 4595, Ap

ALIGNMENTS

RESULT: 1
US-08-750-145A-20
Sequence 20, Application US/08750145A
Patent No. 6010851
GENERAL INFORMATION:
APPLICANT: MIHARA, Yasuhiro
APPLICANT: UTAGAWA, Takashi
APPLICANT: YAMADA, Hideaki
APPLICANT: ASANO, Yasuhisa
TITLE OF INVENTION: Method for Producing Nucleoside-5'-
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESS: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFF. DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750, 145A
FILING DATE: 01-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-149781
FILING DATE: 05-May-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-094680
FILING DATE: 26-Mar-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0830-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Enterobacter aerogenes
STRAIN: IFO 12010

US-08-750-145A-20

Query Match 100.0%; Score 1173; DB 3; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.8e-127;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVPAGNDATTKPDLYYLKNAQAIDSLALLPPEPEVGSIAFLNDQAMYEKGRLLRNTERGK 60
DB 21 LVPAGNDATTKPDLYYLKNAQAIDSLALLPPEPEVGSIAFLNDQAMYEKGRLLRNTERGK 80
QY 61 LAADANLISAGVANAFASSAFSGPITTEKDAPOHLKLTNMI EDAGDLATRSKKEKYMIR 120
DB 81 LAADANLISAGVANAFASSAFSGPITTEKDAPOHLKLTNMI EDAGDLATRSKKEKYMIR 140
QY 121 PFAFYGVSTCNTTEEDDKLSKNGSYSGHTSIGMATLVLAELNPOQNEILKRGYELGES 180
DB 141 PFAFYGVSTCNTTEEDDKLSKNGSYSGHTSIGMATLVLAELNPOQNEILKRGYELGES 200
QY 181 RVICGYHWSQDVDAARIVGSAVAVATLHTNPAFOOQLOKAKDEFAKTOK 228
DB 201 RVICGYHWSQDVDAARIVGSAVAVATLHTNPAFOOQLOKAKDEFAKTOK 248

RESULT 2

US-08-975-698A-24
Sequence 24, Application US/08975698A
Patent No. 6015697
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIKA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P. C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,698A
FILING DATE: 21-NOV-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Enterobacter aerogenes
STRAIN: IFO 12010
US-08-975-698A-24

Query Match 100.0%; Score 1173; DB 3; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.8e-127;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVPAGNDATTKPDLYYLKNAQAIDSLALLPPEPEVGSIAFLNDQAMYEKGRLLRNTERGK 60
DB 21 LVPAGNDATTKPDLYYLKNAQAIDSLALLPPEPEVGSIAFLNDQAMYEKGRLLRNTERGK 80
QY 61 LAADANLISAGVANAFASSAFSGPITTEKDAPOHLKLTNMI EDAGDLATRSKKEKYMIR 120
DB 81 LAADANLISAGVANAFASSAFSGPITTEKDAPOHLKLTNMI EDAGDLATRSKKEKYMIR 140
QY 121 PFAFYGVSTCNTTEEDDKLSKNGSYSGHTSIGMATLVLAELNPOQNEILKRGYELGES 180
DB 141 PFAFYGVSTCNTTEEDDKLSKNGSYSGHTSIGMATLVLAELNPOQNEILKRGYELGES 200
QY 181 RVICGYHWSQDVDAARIVGSAVAVATLHTNPAFOOQLOKAKDEFAKTOK 228
DB 201 RVICGYHWSQDVDAARIVGSAVAVATLHTNPAFOOQLOKAKDEFAKTOK 248

RESULT 3

US-09-417-090-24
Sequence 24, Application US/09417090
Patent No. 6207435
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIKA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P. C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/417,090
FILING DATE: 13-OCT-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE: 21-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Enterobacter aerogenes
STRAIN: IFO 12010
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-417-090-24

Query Match 100.0%; Score 1173; DB 3; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.8e-127;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 21 LVPAQNDATTTPDLYLLKNAQAIDSLALLPPPEVGSIAFLNDQAMYEKRLRNTTERGK 80
Qy 61 LAEDANISAGGVANAFSSAFSGSPITEKDAPOQLHKLNTNMIEDAGDLATRSKAKERYMRIR 120
Db 81 LAEDANISAGGVANAFSSAFSGSPITEKDAPOQLHKLNTNMIEDAGDLATRSKAKERYMRIR 140
Qy 121 PFAPYGVSTCMTTTEODKLSKNGSPSGHTSIGMATLVLAELINPORONEILKRGYELGES 180
Db 141 PFAPYGVSTCMTTTEODKLSKNGSPSGHTSIGMATLVLAELINPORONEILKRGYELGES 200
Qy 181 RVICGYHMQSDVDAAIRIVGSAVVATLHTNPAFOOOLQAKDEFAKTOK 228
Db 201 RVICGYHMQSDVDAAIRIVGSAVVATLHTNPAFOOOLQAKDEFAKTOK 248

RESULT 4

US-09-727-578-24
Sequence 24, Application US/09727578
Patent No. 6355472
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UYAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIRO
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
TITLE OF INVENTION: ESTER
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P. C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/727, 578
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Enterobacter aerogenes
STRAIN: IFO 12010
US-09-727-578-24

Query Match 100.0%; Score 1173; DB 3; Length 248;
Best Local Similarity 100.0%; Pred. No. 1,86-127;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LVPAQNDATTTPDLYLLKNAQAIDSLALLPPPEVGSIAFLNDQAMYEKRLRNTTERGK 60
Db 21 LVPAQNDATTTPDLYLLKNAQAIDSLALLPPPEVGSIAFLNDQAMYEKRLRNTTERGK 80
Qy 61 LAEDANISAGGVANAFSSAFSGSPITEKDAPOQLHKLNTNMIEDAGDLATRSKAKERYMRIR 120

Db 81 LAEDANISAGGVANAFSSAFSGSPITEKDAPOQLHKLNTNMIEDAGDLATRSKAKERYMRIR 140
Qy 121 PFAPYGVSTCMTTTEODKLSKNGSPSGHTSIGMATLVLAELINPORONEILKRGYELGES 180
Db 141 PFAPYGVSTCMTTTEODKLSKNGSPSGHTSIGMATLVLAELINPORONEILKRGYELGES 200
Qy 181 RVICGYHMQSDVDAAIRIVGSAVVATLHTNPAFOOOLQAKDEFAKTOK 228
Db 201 RVICGYHMQSDVDAAIRIVGSAVVATLHTNPAFOOOLQAKDEFAKTOK 248

RESULT 5

US-09-489-039A-7933
Sequence 7933, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709,2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7933
LENGTH: 253
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7933

Query Match 97.1%; Score 1139; DB 4; Length 253;
Best Local Similarity 96.9%; Pred. No. 1,76-123;
Matches 221; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LVPAQNDATTTPDLYLLKNAQAIDSLALLPPPEVGSIAFLNDQAMYEKRLRNTTERGK 60
Db 26 LVPAQNDATTTPDLYLLKNAQAIDSLALLPPPAVGSIAFLNDQAMYEKRLRNTTERGK 85
Qy 61 LAEDANISAGGVANAFSSAFSGSPITEKDAPOQLHKLNTNMIEDAGDLATRSKAKERYMRIR 120
Db 86 LAEDANISAGGVANAFSSAFSGSPITEKDAPOQLHKLNTNMIEDAGDLATRSKAKERYMRIR 145
Qy 121 PFAPYGVSTCMTTTEODKLSKNGSPSGHTSIGMATLVLAELINPORONEILKRGYELGES 180
Db 146 PFAPYGVSTCMTTTEODKLSKNGSPSGHTSIGMATLVLAELINPORONEILKRGYELGES 205
Qy 181 RVICGYHMQSDVDAAIRIVGSAVVATLHTNPAFOOOLQAKDEFAKTOK 228
Db 206 RVICGYHMQSDVDAAIRIVGSAVVATLHTNPAFOOOLQAKDEFAKTOK 253

RESULT 6

US-08-750-145A-22
Sequence 22, Application US/08750145A
Patent No. 6010851
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UYAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIRO
TITLE OF INVENTION: Method for Producing Nucleoside-5'-
TITLE OF INVENTION: Phosphate Ester
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P. C.
STREET: 1755 S. JEFF. DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,145A
FILING DATE: 01-JAN-1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 7-149781
FILING DATE: 05-May-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-094680
FILING DATE: 26-Mar-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0830-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Klebsiella planticola
STRAIN: IFO 14939
US-08-750-145A-22

Query Match 96.8%; Score 1136; DB 3; Length 248;
Best Local Similarity 96.9%; Pred. No. 3 6e-123;
Matches 221; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 LVPAAGDATTTPDLYLKNAQAIIDSLALPPPEVGSIAFLNDQAMYEKRLRATERGK 60
DB 21 LVPAAGDATTTPDLYLKNAQAIIDSLALPPPEVGSIAFLNDQAMYEKRLRATERGK 80
QY 61 LAEDANLSAGGVANNAFSAFSGSPITEKDAFOLHKLITNMIEDAGDLATRSAREKYMIR 120
DB 81 LAEDANLSAGGVANNAFSAFSGSPITEKDAFOLHKLITNMIEDAGDLATRSAREKYMIR 140
QY 121 PFAFYGVSTCTTTEODKLSKNGSYPSGHTSIGMATLVLAELINPQRONEILKRGYELGES 180
DB 141 PFAFYGVSTCTTTEODKLSKNGSYPSGHTSIGMATLVLAELINPQRONEILKRGYELGES 200
QY 181 RVICGYHMOSDVDAARIVGSAVVAATLHTNPAFOOQLOKAKDEFKAKOK 228
DB 201 RVICGYHMOSDVDAARIVGSAVVAATLHTNPAFOOQLOKAKDEFKAKOK 248

RESULT 7
US-08-975-698A-26
Sequence 26, Application US/08975698A
Patent No. 6015697
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
TITLE OF INVENTION: ESTER
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
APPLICATION NUMBER: US/08975698A

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,698A
FILING DATE: 21-NOV-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Klebsiella planticola
STRAIN: IFO 14939
US-08-975-698A-26

Query Match 96.8%; Score 1136; DB 3; Length 248;
Best Local Similarity 96.9%; Pred. No. 3 6e-123;
Matches 221; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 LVPAAGDATTTPDLYLKNAQAIIDSLALPPPEVGSIAFLNDQAMYEKRLRATERGK 60
DB 21 LVPAAGDATTTPDLYLKNAQAIIDSLALPPPEVGSIAFLNDQAMYEKRLRATERGK 80
QY 61 LAEDANLSAGGVANNAFSAFSGSPITEKDAFOLHKLITNMIEDAGDLATRSAREKYMIR 120
DB 81 LAEDANLSAGGVANNAFSAFSGSPITEKDAFOLHKLITNMIEDAGDLATRSAREKYMIR 140
QY 121 PFAFYGVSTCTTTEODKLSKNGSYPSGHTSIGMATLVLAELINPQRONEILKRGYELGES 180
DB 141 PFAFYGVSTCTTTEODKLSKNGSYPSGHTSIGMATLVLAELINPQRONEILKRGYELGES 200
QY 181 RVICGYHMOSDVDAARIVGSAVVAATLHTNPAFOOQLOKAKDEFKAKOK 228
DB 201 RVICGYHMOSDVDAARIVGSAVVAATLHTNPAFOOQLOKAKDEFKAKOK 248

RESULT 8
US-09-417-090-26
Sequence 26, Application US/09417090
Patent No. 6207435
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
TITLE OF INVENTION: ESTER
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
APPLICATION NUMBER: US/09417090

FILING DATE: 13-Oct-1999
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/975,698
 FILING DATE: 21-NOV-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: OBLON, NORMAN F
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 0010-0885-0
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 413-3000
 TELEFAX: (703) 413-2220
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 248 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 ORGANISM: Klebsiella planticola
 STRAIN: IFO 14939
 SEQUENCE DESCRIPTION: SEQ ID NO: 26:
 US-09-417-090-26

Query Match 96.8%; Score 1136; DB 3; Length 248;
 Best Local Similarity 96.9%; Pred. No. 3.6e-123;
 Matches 221; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 LVPAGNDATTKPDLYLLKNAQAIDSLALPPPEVGSIAFLINDQAMYEKGRLLRTERGK 60
 DB 21 LVPAGNDATTKPDLYLLKNAQAIDSLALPPPEVGSIAFLINDQAMYEKGRLLRTERGK 80
 QY 61 LAADANLSAGVANAFSAFSGSPITEKDAFOLHKLNTMIEDAGDLATRSKKEKYMIR 120
 DB 81 LAADANLSAGVANAFSAFSGSPITEKDAFOLHKLNTMIEDAGDLATRSKKEKYMIR 140
 QY 121 PFAFYGVSTCMTTEODKLSKNGSYPSGHTSIGMATLVLAETINPORONEILKRGYELGES 180
 DB 141 PFAFYGVSTCMTTEODKLSKNGSYPSGHTSIGMATLVLAETINPORONEILKRGYELGES 200
 QY 181 RVICGYHMQSDVDARIIVGSAVATLHTNPAFQOOLQAKDEFAKQK 228
 DB 201 RVICGYHMQSDVDARIIVGSAVATLHTNPAFQOOLQAKDEFAKQK 248

RESULT 9
 US-09-727-578-26
 Sequence 26, Application US/09727578
 Patent No. 6355472
 GENERAL INFORMATION:
 APPLICANT: MIHARA, YASUHIRO
 APPLICANT: UTAGAWA, TAKASHI
 APPLICANT: YAMADA, HIDEAKI
 APPLICANT: ASANO, YASUHISA
 TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
 STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: USA
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/727,578
 FILING DATE:
 CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/975,698
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: OBLON, NORMAN F
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 0010-0885-0
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 413-3000
 TELEFAX: (703) 413-2220
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 248 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 ORGANISM: Klebsiella planticola
 STRAIN: IFO 14939
 US-09-727-578-26

Query Match 96.8%; Score 1136; DB 3; Length 248;
 Best Local Similarity 96.9%; Pred. No. 3.6e-123;
 Matches 221; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 LVPAGNDATTKPDLYLLKNAQAIDSLALPPPEVGSIAFLINDQAMYEKGRLLRTERGK 60
 DB 21 LVPAGNDATTKPDLYLLKNAQAIDSLALPPPEVGSIAFLINDQAMYEKGRLLRTERGK 80
 QY 61 LAADANLSAGVANAFSAFSGSPITEKDAFOLHKLNTMIEDAGDLATRSKKEKYMIR 120
 DB 81 LAADANLSAGVANAFSAFSGSPITEKDAFOLHKLNTMIEDAGDLATRSKKEKYMIR 140
 QY 121 PFAFYGVSTCMTTEODKLSKNGSYPSGHTSIGMATLVLAETINPORONEILKRGYELGES 180
 DB 141 PFAFYGVSTCMTTEODKLSKNGSYPSGHTSIGMATLVLAETINPORONEILKRGYELGES 200
 QY 181 RVICGYHMQSDVDARIIVGSAVATLHTNPAFQOOLQAKDEFAKQK 228
 DB 201 RVICGYHMQSDVDARIIVGSAVATLHTNPAFQOOLQAKDEFAKQK 248

RESULT 10
 US-08-750-145A-11
 Sequence 11, Application US/08750145A
 Patent No. 6010851
 GENERAL INFORMATION:
 APPLICANT: MIHARA, Yasuhiro
 APPLICANT: UTAGAWA, Takashi
 APPLICANT: YAMADA, Hideaki
 APPLICANT: ASANO, Yasuhisa
 TITLE OF INVENTION: Method for Producing Nucleoside-5'-
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
 STREET: 1755 S. JEFF. DAVIS HIGHWAY, SUITE 400
 CITY: ARLINGTON
 STATE: VA
 COUNTRY: USA
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/750,145A
 FILING DATE: 01-JAN-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-149781
 FILING DATE: 05-May-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-094680
FILING DATE: 26-Mar-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0830-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE: Escherichia blattae
STRAIN: JCM 1650
US-08-750-145A-11

Query Match 93.0%; Score 1091; DB 3; Length 231;
Best Local Similarity 92.1%; Pred. No. 5.3e-118;
Matches 210; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 LVPAQNDATTKPDLYYLKNAQAIDSLALPPPEVGSIAFLNDQAMYEKRLNTERGK 60
DB 3 LVATGNDTTPKPDLYYLKNSSEALNSLALPPPAVGSIAFLNDQAMYEKRLNTERGK 62
QY 61 LAEDANLSAGVANAFSSAFSGPITEKAPALHKLNTMTEDAGDLATRSAREKMYRIR 120
DB 63 LAEDANLSAGVANAFSSAFSGPITEKAPALHKLNTMTEDAGDLATRSAREKMYRIR 122
QY 121 PFAFYGVSTCNTTEODKLSKNGSPSGHTSIGMATLVLAELNFORONEILKRGYELGS 180
DB 123 PFAFYGVSTCNTTEODKLSKNGSPSGHTSIGMATLVLAELNFORONEILKRGYELGS 182
QY 181 RVICGYHWSQDVDAARIVGSAVVATLHTNPAFQOOLQAKADEFAKTK 228
DB 183 RVICGYHWSQDVDAARIVGSAVVATLHTNPAFQOOLQAKADEFAKTK 230

RESULT 11

US-08-975-698A-8
Sequence 8, Application US/08975698A
Patent No. 6015697
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIRO
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,698A
FILING DATE: 21-NOV-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE: Escherichia blattae
STRAIN: JCM 1650
US-08-975-698A-8

Query Match 93.0%; Score 1091; DB 3; Length 231;
Best Local Similarity 92.1%; Pred. No. 5.3e-118;
Matches 210; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 LVPAQNDATTKPDLYYLKNAQAIDSLALPPPEVGSIAFLNDQAMYEKRLNTERGK 60
DB 3 LVATGNDTTPKPDLYYLKNSSEALNSLALPPPAVGSIAFLNDQAMYEKRLNTERGK 62
QY 61 LAEDANLSAGVANAFSSAFSGPITEKAPALHKLNTMTEDAGDLATRSAREKMYRIR 120
DB 63 LAEDANLSAGVANAFSSAFSGPITEKAPALHKLNTMTEDAGDLATRSAREKMYRIR 122
QY 121 PFAFYGVSTCNTTEODKLSKNGSPSGHTSIGMATLVLAELNFORONEILKRGYELGS 180
DB 123 PFAFYGVSTCNTTEODKLSKNGSPSGHTSIGMATLVLAELNFORONEILKRGYELGS 182
QY 181 RVICGYHWSQDVDAARIVGSAVVATLHTNPAFQOOLQAKADEFAKTK 228
DB 183 RVICGYHWSQDVDAARIVGSAVVATLHTNPAFQOOLQAKADEFAKTK 230

RESULT 12

US-09-417-090-8
Sequence 8, Application US/09417090
Patent No. 6207435
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIRO
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/417,090
FILING DATE: 13-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE: 21-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Escherichia blattae
STRAIN: JCM 1650
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-417-090-8

Query Match 93.0%; Score 1091; DB 3; Length 231;
Best Local Similarity 92.1%; Pred. No. 5,3e-118;
Matches 210; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 LVPAQNDATTKPDLYLLKNAQAIDSLALPPPEVGSIAFLNDQAMYEKGRLLRTERGK 60
DB 3 LVATNDTTTKPDLYLLKNSBAINSLALPPPAVGSIAFLNDQAMYEGRLLRTERGK 62

QY 61 LAEPDANISAGVANAFSAGFSPITEKAPOLHKLITNMIEDAGDLATRSKAKYMRIR 120
DB 63 LAEPDANISAGVANAFSAGFSPITEKAPALHKLITNMIEDAGDLATRSKADHYMRIR 122

QY 121 PPAFYGVSTCWTTEQDKLSKNGSYSPGHTSIGMATLVLAEPORONEILKRGYELGS 180
DB 123 PPAFYGVSTCWTTEQDKLSKNGSYSPGHTSIGMATLVLAEPORONEILKRGYELGS 182

QY 181 RVICGYHMQSDVDARIVGSAVVATLHTNPAFQOOLQAKADEFAKTOK 228
DB 183 RVICGYHMQSDVDARIVGSAVVATLHTNPAFQOOLQAKADEFAKHOK 230

RESULT 13
US-09-727-578-8
Sequence 8, Application US/09727578
Patent No. 6355472
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
TITLE OF INVENTION: ESTER
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/727,578
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Escherichia blattae
STRAIN: JCM 1650
US-09-727-578-8

Query Match 93.0%; Score 1091; DB 3; Length 231;
Best Local Similarity 92.1%; Pred. No. 5,3e-118;
Matches 210; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 LVPAQNDATTKPDLYLLKNAQAIDSLALPPPEVGSIAFLNDQAMYEKGRLLRTERGK 60
DB 3 LVATNDTTTKPDLYLLKNSBAINSLALPPPAVGSIAFLNDQAMYEGRLLRTERGK 62

QY 61 LAEPDANISAGVANAFSAGFSPITEKAPOLHKLITNMIEDAGDLATRSKAKYMRIR 120
DB 63 LAEPDANISAGVANAFSAGFSPITEKAPALHKLITNMIEDAGDLATRSKADHYMRIR 122

QY 121 PPAFYGVSTCWTTEQDKLSKNGSYSPGHTSIGMATLVLAEPORONEILKRGYELGS 180
DB 123 PPAFYGVSTCWTTEQDKLSKNGSYSPGHTSIGMATLVLAEPORONEILKRGYELGS 182

QY 181 RVICGYHMQSDVDARIVGSAVVATLHTNPAFQOOLQAKADEFAKTOK 228
DB 183 RVICGYHMQSDVDARIVGSAVVATLHTNPAFQOOLQAKADEFAKHOK 230

RESULT 14
US-08-750-145A-10
Sequence 10, Application US/08750145A
Patent No. 6010851
GENERAL INFORMATION:
APPLICANT: MIHARA, Yasuhiro
APPLICANT: UTAGAWA, Takashi
APPLICANT: YAMADA, Hideaki
APPLICANT: ASANO, Yasuhisa
TITLE OF INVENTION: Method for Producing Nucleoside-5'-
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFF. DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,145A
FILING DATE: 01-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-149781
FILING DATE: 05-May-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-094680
FILING DATE: 26-Mar-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0830-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Escherichia blattae
STRAIN: JCM 1650
US-08-750-145A-10

Query Match 93.0%; Score 1091; DB 3; Length 249;
Best Local Similarity 92.1%; Pred. No. 5.9e-118;
Matches 210; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 LVPAQNDATTKPDLYYLKNAQAIDSLALPPPEVGSIAFLNDQAMEKGRLLRTERGK 60
DB 21 LVATGNDTTTKPDLYYLKNSAINSLLALPPPAVGSIAFLNDQAMEQRLRTERGK 80
QY 61 LAEDANLSAGGVANAFSSAFSGSPITEKDAPOHLKLTNMIEDAGDLATRSADHYMRIR 120
DB 81 LAEDANLSAGGVANAFSSAFSGSPITEKDAPOHLKLTNMIEDAGDLATRSADHYMRIR 140
QY 121 PPAFYGVSTCNTTEBODKLSKNGSYPSGHTSIGMATLVLAEPORONEILKRGYELGES 180
DB 141 PPAFYGVSTCNTTEBODKLSKNGSYPSGHTSIGMATLVLAEPORONEILKRGYELGES 200
QY 181 RVICGYHMQSDVDARIVGSAVVATLTHTNPAFOOQLOKAKDEFAPQHOX 228
DB 201 RVICGYHMQSDVDARIVGSAVVATLTHTNPAFOOQLOKAKDEFAPQHOX 248

RESULT 15
US-08-975-698A-7
Sequence 7, Application US/08975698A
Patent No. 6015697

GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSER: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,698A
FILING DATE: 21-NOV-1997
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:

ORGANISM: Escherichia blattae
STRAIN: JCM 1650
US-08-975-698A-7

Query Match 93.0%; Score 1091; DB 3; Length 249;
Best Local Similarity 92.1%; Pred. No. 5.9e-118;
Matches 210; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 LVPAQNDATTKPDLYYLKNAQAIDSLALPPPEVGSIAFLNDQAMEKGRLLRTERGK 60
DB 21 LVATGNDTTTKPDLYYLKNSAINSLLALPPPAVGSIAFLNDQAMEQRLRTERGK 80
QY 61 LAEDANLSAGGVANAFSSAFSGSPITEKDAPOHLKLTNMIEDAGDLATRSADHYMRIR 120
DB 81 LAEDANLSAGGVANAFSSAFSGSPITEKDAPOHLKLTNMIEDAGDLATRSADHYMRIR 140
QY 121 PPAFYGVSTCNTTEBODKLSKNGSYPSGHTSIGMATLVLAEPORONEILKRGYELGES 180
DB 141 PPAFYGVSTCNTTEBODKLSKNGSYPSGHTSIGMATLVLAEPORONEILKRGYELGES 200
QY 181 RVICGYHMQSDVDARIVGSAVVATLTHTNPAFOOQLOKAKDEFAPQHOX 228
DB 201 RVICGYHMQSDVDARIVGSAVVATLTHTNPAFOOQLOKAKDEFAPQHOX 248

Search completed: March 2, 2005, 20:28:51
Job time: 30.8039 secs

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OM protein - protein search, using sw model

Run on: March 2, 2005, 20:15:51 ; Search time 25.333 Seconds
(without alignments)
865.951 Million cell updates/sec

Title: US-09-807-990A-125

Perfect score: 1173

Sequence: 1 LVPAGNDATTKRPDIYYLKNA.....NPAFQQLQAKADEFAKTOK 228

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1035	88.2	248	1	PAOFCS
2	983.5	83.8	249	1	acid phosphatase (
3	483	41.2	250	1	acid phosphatase (
4	476.5	40.6	250	2	acid phosphatase (
5	341.5	29.1	264	1	acid phosphatase (
6	274.5	23.4	258	2	acid phosphatase (
7	186	15.9	2314	2	acid phosphatase (
8	161	13.7	241	2	probable acid phos
9	151	12.9	591	2	uncharacterized pr
10	147	12.5	660	2	serine proteinase
11	147	12.5	660	2	vanadium chloroper
12	105	9.0	145	2	conserved hypotet
13	98.5	8.4	259	2	conserved hypotet
14	96	8.2	178	2	seed biotin-contai
15	93.5	8.0	643	1	hypothetical prote
16	92	7.8	217	2	conserved hypotet
17	92	7.8	242	2	vacb-like (shlgel)
18	91.5	7.8	725	2	P element - fruit
19	90.5	7.7	562	2	hypothetical prote
20	90	7.7	437	2	hypothetical prote
21	89	7.6	608	2	protein B0205.3 (1
22	88.5	7.5	1707	2	hypothetical prote
23	87	7.4	292	2	phosphatidylglycer
24	86	7.3	525	2	conserved hypotet
25	85.5	7.3	514	2	25-hydroxyvitamin
26	85	7.2	766	2	P element transpos
27	84.5	7.2	921	2	Na+/Ca2+-exchang
28	84.5	7.2	1261	2	hypothetical prote
29	84	7.2	1588	2	probable adhesin 2

30	84	7.2	1588	2	H91188	probable adhesin E
31	84	7.2	3746	1	YGPLV3	alpha-aminoadipyl-
32	84	7.2	3791	1	YGPLV8	hypothetical prote
33	83.5	7.1	320	2	AE2020	hypothetical prote
34	83.5	7.1	589	2	T29897	hypothetical prote
35	83	7.1	253	2	AB0271	phosphatidylglycer
36	83	7.1	493	2	PS0157	MDM10 protein - ye
37	83	7.1	753	2	S22802	transposase (clone
38	82.5	7.0	292	1	CS5070	3',5'-cyclic-nucle
39	82.5	7.0	292	2	CS5070	hypothetical prote
40	82.5	7.0	498	2	CS7551	glutamy1-cRNA (Gln)
41	82.5	7.0	514	2	S60033	25-hydroxyvitamin
42	82.5	7.0	721	2	S31820	gene Mx protein -
43	82.5	7.0	721	2	A37472	interferon-inducib
44	82	7.0	202	2	A82076	conserved hypotet
45	82	7.0	218	2	B97497	22k outer membrane

ALIGNMENTS

RESULT 1

PAOFCS

acid phosphatase (EC 3.1.3.2) - Providencia stuartii

C:Species: Providencia stuartii

C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004

C:Accession: S19888

R:Riccio, M.L., Lombardi, G., Chiesurin, A., Satta, G.

Submitted to the EMBL Data Library, February 1992

A:Reference number: S19888

A:Accession: S19888

A:Molecule type: DNA

A:Residues: 1-248 <R1C>

A:Cross-references: UNIPROT:P26975; EMBL:X64820; NID:g45861; PIDN:CAA46032.1; PID:g45862

C:Genetics:

A:Gene: phoN

C:Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic do

C:Keywords: phosphoric monoster hydrolase.

P:103-222/Domain: glucose-6-phosphatase catalytic domain homology <GN>

Query Match 88.2%; Score 1035; DB 1; Length 248;

Best Local Similarity 85.5%; Pred. No. 1.5e-82;

Matches 194; Conservative 20; Mismatches 13; Indels 0; Gaps 0;

QY	2	VPAQNDATTKRPDIYYLKNAQIDSLALPPPEVGSIAFLNDQMYEGRLLRTERGKL	61
DB	22	IPPGNDVTTKPDLYLLKNSQALIDSLALPPPEVGSILFLNDQMYEGRLLRTERGEQ	81
QY	62	AAEDANLSAGGVANAFSSAFSGPITTEKDAPOHLKLTNMIEDAGDLATRSAREKYMRIIP	121
DB	82	AAKADADLAGGVANAFSEAFSGPITTEKDAPEIHLKLTNMIEDAGDLATRSAREKYMRIIP	141
QY	122	PAFYGVSTCNTTEODKLSKNGSYPSGHTSIGMATVLAELINPQONEILKRGYELGSR	181
DB	142	FAFYGVATCNTKQDDKLSKNGSYSGHTAIGMASVALVSEINPNQDKILKRGYELGSR	201
QY	182	VICGYHWQSDVDARIVGSAVATLTNPAFOQLQAKDEFAKTOK	228
DB	202	VICGYHWQSDVDARIVASGAVATLTNSNPEFOQLQAKDEFAKTOK	248

RESULT 2

S19187

acid phosphatase (EC 3.1.3.2) - Morganella morganii

C:Species: Morganella morganii

C:Date: 28-Jan-2000 #sequence_revision 28-Jan-2000 #text_change 09-Jul-2004

C:Accession: S19187

R:Thaler, M.C.; Berluti, F.; Schippa, S.; Rosolini, G.M.

Submitted to the EMBL Data Library, February 1992

A:Description: Sequencing the Morganella morganii phoC gene coding for a periplasmic ac

A:Reference number: S19187

A:Accession: S19187

A:Molecule type: DNA

A:Residues: 1-249 <THA>
A:Cross-references: UNIPROT:P26581; EMBL:X64444; NID:944463; PIDN:CAA5774.1; PID:944464
C:Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic do
C:Keywords: phosphoric monoester hydrolase
F:109-222/Domain: glucose-6-phosphatase catalytic domain homology <GPH>

Query Match 83.8%; Score 983.5; DB 1; Length 249;
Best Local Similarity 82.9%; Pred. No. 4,5e-78;
Matches 189; Conservative 16; Mismatches 22; Indels 1; Gaps 1;

QY 2 VPAGNDATTTKPDLYLKNQAQIDSLALPPPEVGSIAFLNDQAMYEKRLANTERGL 61
DB 22 IIPANDATTTKPDLYLKNQAQIDSLALPPPEVGSIAFLNDQAMYEKRLANTERGL 81
QY 62 AADANASAGVANAFSSAFSGPTTEKDAPOHLKLTNMIEDAGDLATRSKAKYRIRP 121
DB 82 AOADADLAAGGVATRSAGATGPTTEKDSPELYKLTNMIEDAGDLATRSKAKYRIRP 141
QY 122 PAFYGVSTCNTTTEODKLSKNGSYPSGHTSIGMATVLAELINPORONEILKRGYELGESR 181
DB 142 FAFYGVSTCNTTTEODKLSKNGSYPSGHTSIGMATVLAELINPORONEILKRGYELGESR 201
QY 182 VIGYHMQSDVDARIVGSAVVAITHTNPAFOOLQAKDEPA-KTQK 228
DB 202 VIGYHMQSDVDARIVGSAVVAITHTNPAFOOLQAKDEPA-KTQK 249

RESULT 3

A41330
acid phosphatase (EC 3.1.3.2) Phos precursor - Salmonella typhimurium
N:Alternate names: glycerophosphatase; nonspecific acid phosphatase; phosphomonoesterase
C:Species: Salmonella typhimurium
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S20958; A41330; S14515; S18926
R:Grossman, E.A.; Saier Jr., M.H.; Ochman, H.
EMBO J. 11, 1309-1316, 1992
A:Title: Horizontal transfer of a phosphatase gene as evidence for mosaic structure of t
A:Reference number: S20958; MUID:92224869; PMID:1339343
A:Accession: S20958
A:Molecule type: DNA
A:Residues: 1-250 <GRO>
A:Cross-references: UNIPROT:P26976; EMBL:X63599; NID:947823; PIDN:CAA45144.1; PID:947824
R:Kashihara, M.; Nakata, A.; Shingawa, H.
J. Bacteriol. 173, 6760-6765, 1991
A:Title: Molecular analysis of the Salmonella typhimurium phoN gene, which encodes nonsp
A:Reference number: A41330; MUID:92041557; PMID:1938882
A:Accession: A41330
A:Molecule type: DNA
A:Residues: 1-228, 'SVRS' <KAS>
A:Cross-references: GB:X59036; NID:948894; PIDN:CAA11760.1; PID:948895
C:Genetics:
A:Gene: phoN
A:Map position: 96 min
A>Note: regulated by the two-component regulatory system consisting of phoP and phoQ
C:Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic do
C:Keywords: periplasmic space; phosphoric monoester hydrolase
F:108-221/Domain: glucose-6-phosphatase catalytic domain homology <GPH>

Query Match 41.2%; Score 483; DB 1; Length 250;
Best Local Similarity 47.0%; Pred. No. 1.6e-34;
Matches 95; Conservative 33; Mismatches 74; Indels 0; Gaps 0;

QY 21 QAIDSLALPPPEVGSIAFLNDQAMYEKRLANTERGLAABDANISAGVANAFSSA 80
DB 31 ESNVSGFLLPPPPGNDPAVRYDEAVFKGYAIFKQSPMKQAAEDADVSVENIRIFSPV 90
QY 81 FGSDITEKDAPOHLKLTNMIEDAGDLATRSKAKYRIRFPAFVYSTCNTTEODKLSK 140
DB 91 VGAKINPDTEETNMKLLTMGYYATAKAKYKTRTFVYFNHSTCKPEDENTLRK 150
QY 141 NGSYPSGHTSIGMATVLAELINPORONEILKRGYELGESRIVIGYHMQSDVDARIVGS 200
DB 151 NGSYPSGHTSIGMATVLAELINPORONEILKRGYELGESRIVIGYHMQSDVDARIVGS 210

QY 201 AVATLHTNPAFOOLQAKDE 222
DB 211 VEFARLQITIPAFQKSLAKVREE 232

RESULT 4

AF1025
acid phosphatase (EC 3.1.3.2) - Salmonella enterica subsp. enterica serovar Typhi (strain
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A>Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 25-Aug-2003
C:Accession: AF1025
R:Parhill, D.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AF1025
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-250 <PAR>
A:Cross-references: GB:A513382; PIDN:CAD09303.1; PID:916505305; GSPDB:GN00176
C:Genetics:
A:Gene: phoN
C:Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic do
C:Keywords: phosphoric monoester hydrolase

Query Match 40.6%; Score 476.5; DB 2; Length 250;
Best Local Similarity 44.7%; Pred. No. 5.7e-34;
Matches 96; Conservative 37; Mismatches 79; Indels 3; Gaps 1;

QY 8 ATTPDLYLKNQAQIDSLALPPPEVGSIAFLNDQAMYEKRLANTERGLAABDAN 67
DB 21 ATMPD---FSPBSVNSQFYLLPPPGNDPAVRYDEAVFKGYALKGSRMKQAAEDAD 77
QY 68 LSAAGVANAFSSAFSGPTTEKDAPOHLKLTNMIEDAGDLATRSKAKYRIRPFAFYGV 127
DB 78 ISEVNIARIFSPVGAATKPDTEETNMKLLTMGYYATAKAKYKTRTFVYFNH 137
QY 128 STCNTTEODKLSKNGSYPSGHTSIGMATVLAELINPORONEILKRGYELGESRIVCGH 187
DB 138 STCKPEDENTLRKDSGTPSGHTYITLALVLSQAPRQELARKGMEFGOSRVICGAH 197
QY 188 WQSDVDARIVGSAVVAITHTNPAFOOLQAKDE 222
DB 198 WQSDVDAGRYGAVEFARLQITIPAFQKSLAKVREE 232

RESULT 5

A32044
acid phosphatase (EC 3.1.3.2) - Zymomonas mobilis
C:Species: Zymomonas mobilis
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A32044
R:Pond, J.L.; Eddy, C.K.; Mackenzie, K.F.; Conway, T.; Borecky, D.J.; Ingram, L.O.
J. Bacteriol. 171, 767-774, 1989
A:Title: Cloning, sequencing, and characterization of the principal acid phosphatase, the
A:Reference number: A32044; MUID:89123152; PMID:2914872
A:Accession: A32044
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-264 <PON>
A:Cross-references: UNIPROT:P14924; GB:M24141; NID:9155613; PIDN:AAA27700.1; PID:9155614
C:Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic do
C:Keywords: phosphoric monoester hydrolase
F:99-212/Domain: glucose-6-phosphatase catalytic domain homology <GPH>

Query Match 29.1%; Score 341.5; DB 1; Length 264;
Best Local Similarity 36.8%; Pred. No. 3.4e-22;
Matches 75; Conservative 31; Mismatches 97; Indels 1; Gaps 1;

QY 24 DSLALLPPEVSGIAFLNDQAMYEKGRLLRNTBGRKLAEDNLSAGVANAFSSAFGS 83
DB 44 DPLVLIAPPPTSGSPLOAHDDDTFNSTROLKSGTRKALMTQDADHLAVALKDYACAGM 103
QY 84 PITEKADPOLHKLITNMIEDAGDLATRSAREKMYRIRPAFYGVSTCNTTEODKLSKNGS 143
DB 104 NLDIAQLPHLANLIKRAKARTEYDIDIGR-AKNNMNRKRPFDVTDQPICTEKDEKREGKQGS 162
QY 144 YPSGHTSIGMATLVLAELNFORONEILKRGYELGSRVICYGHWSQDVDAARIYGSAAV 203
DB 163 YPSGHTTIGMSVALILAEILIPDHANILIORGOIFGTSRIVCGAHWFSDVQAGYIMASGEI 222
QY 204 ATLHTNPAFOOOLQAKDEFAKTO 227
DB 223 AALHGADFRDMELARKLELEKAR 246

RESULT 6

acid phosphatase [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 25-Aug-2003
C:Accession: E87293
R:NIEMAN, M.C.; FELDBLYUM, T.V.; PAULSEN, I.T.; NELSON, K.E.; EISEN, J.; HEIDELBERG, J.
B.; LAUB, M.T.; DEBOY, R.T.; DODSON, R.J.; DURKIN, A.S.; GWINN, M.L.; HAFT, D.H.; KOJON
N, J.; EMOJAEVA, M.; WHITE, O.; SALZBERG, S.L.; SHAPIRO, L.; VENTER, J.C.; FRASER, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: E87293
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <STO>
A:Cross-references: GB:AE005673; NID:g13421511; PIDN:AAK22345.1; GSPDB:GN00148
A:Genetics:
A:Gene: CC0358
C:Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic do

Query Match 23.4%; Score 274.5; DB 2; Length 258;
Best Local Similarity 36.3%; Pred. No. 2.2e-16;
Matches 77; Conservative 31; Mismatches 97; Indels 7; Gaps 7;
QY 12 PDLVYLKNAQATDSLALLPPEVSGIAFLNDQAMYEKGRLLRNTBGRKLAEDNLSAG 71
DB 25 PSNRVLANG-VFDADHLPPEPAKSGEALRDRERFRAIRALKDTPRMSLAGEQ-NVEE- 81
QY 72 GVANAFSSAFG-SPITEKADPOLHKLITNMIEDAGDLATRSAREKMYRIRPAFYGVSTC 130
DB 82 KYLDGACALGVTPSPFERI-PKLAATVILRMSRDVS-AVAGPKLTKRRRPFIFSEGPIC 139
QY 131 NTEODKLSKNGSYSGHTSIGMATLVLAELNFORONEILKRGYELGSRVICYGHWS 190
DB 140 -IKRSLGLALSPDPSGHATWMSVGLVLAEPDRRAILARAQYGSRYVVCVHNMS 198
QY 191 DYDAARIVGSAAVATLHTNPAFOOOLQAKDE 222
DB 199 SVEAGRMNAENLISALKSSDAFKADLAARAE 230

RESULT 7

hypothetical protein - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T28698
R:Parkhill, J.; Bentley, S.D.; Barrett, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, January 1999
A:Reference number: Z20512
A:Accession: T28698
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2314 <PAR>

A:Cross-references: UNIPROT:O69822; EMBL:AL023496; NID:e1292348; PID:e1292365; PIDN:CAAL
Query Match 15.9%; Score 186; DB 2; Length 2314;
Best Local Similarity 31.0%; Pred. No. 2.1e-07;
Matches 53; Conservative 26; Mismatches 78; Indels 14; Gaps 5;

QY 62 AAEDNLS-AGVANAFSSAFSGPITEKADPOLHKLITNMIE--DAGDLATRSAREKMYR 118
DB 1878 ASNSATVTMMADGSLRGLPVLGEALKEGRLEKTSALFRVENVENDTHD-----AAKNHGY 1933
QY 119 IRPF---APYGVSTCNTTEODK---LSKNGSYSGHTSIGMATLVLAELNFORONEIL 171
DB 1934 LRPLYRLGAFGCGAVYESQDSYSGLAGQSSYPSGHTYGGVEAGTITATLLPDLAPSL 1993
QY 172 KRGYELGSRVICYGHWSQDVDAARIYGSAAVATLHTNPAFOOOLQAKDE 222
DB 1994 ARTSEYGDNRIVLGFHYPLDVWGGRITQAATVAHRMADPEPAKLGQAHT 2044

RESULT 8

probable acid phosphatase PA0190 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 25-Aug-2003
C:Accession: C63621
R:STORER, C.K.; PHAM, X.O.; ERWIN, A.L.; MIZOGUCHI, S.D.; WARENER, P.; HICKEY, M.J.; BR
ADMAN, S.; YUAN, Y.; BRODY, L.L.; COULTER, S.N.; FOLGER, K.R.; KAS, A.; LARZIG, K.; LIM,
J.; LOY, S.; OLSON, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho-
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: C63621
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-241 <STO>
A:Cross-references: GB:AE004457; GB:AE004091; NID:g9946024; PIDN:AAQ03580.1; GSPDB:GN001
A:Experimental source: strain PA01
A:Genetics:
A:Gene: PA0190
C:Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic do

Query Match 13.7%; Score 161; DB 2; Length 241;
Best Local Similarity 26.5%; Pred. No. 1.5e-06;
Matches 54; Conservative 36; Mismatches 88; Indels 26; Gaps 7;
QY 29 LPPEVSGIAFLNDQAMYEKGRLLRNTBGRKLAEDNLSAGVANAFSSAFG 82
DB 43 LPPEPAADSAALVADLGAVALRQRLRPEQVRVRAHDQWEDNVPFAGDILGASFDKER 102
QY 83 SPITEKADPOLHKLITNMIEDAGDLATRSAREKMYRIRPAFYGVSTCNTTEODK---L 138
DB 103 LPLTRS---FNNRAQENIVE-----VIMPAKHFAPRRPY-----EVTRKVRVLRP 146
QY 139 SKNGSYSGHTSIGMATLVLAELNFORONEILKRGYELGSRVICYGHWSQDVDAARIV 198
DB 147 PEGSYPSGHTMDSTFKASLSMLVPEKNDAPFAAEHNSKRYLAGVHFFSDELGQTA 206
QY 199 GSAAVATLHTNPAFOOOLQAKDE 222
DB 207 AALVAVSLADPAVAADPAVAREE 230

RESULT 9

uncharacterized protein, containing probable phosphatase domain [imported] - Clostridium
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: C66991
R:Noelling, U.; Breton, G.; Omeichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: C96991
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-591 <KUR>
A:Cross-references: UNIPROT:Q97124; GB:AE001437; PIDN:AAK78718.1; PID:g15023624; GSPDB:C
A:Experimental source: Clostridium acetobutylicum ATCC624
C:Genetics:
A:Gene: CAC0742

Query Match 12.9%; Score 151; DB 2; Length 591;
Best Local Similarity 27.2%; Pred. No. 3.8e-05;
Matches 55; Conservative 27; Mismatches 72; Indels 48; Gaps 8;

QY 39 AFINDQAMYEKGRLLRTERGKLA---EDANISAGVNAFSSAGSPITE---KDAI 91
DB 113 AYLDNR-----RNGNSVLDGLGPKDAFKAGCA-----GTTTVDIIPDAI 155
QY 92 QLN-----KLTNMIEDAGDI-----ATRSKEXKMRIRPPAFYG-VSTC 130
DB 156 NVOYTDKGNMAGNNAEESDLSGVKLVDTIRNSAATTPAKONYKYPFRWRMSDKKVL 215
QY 131 NTRQDKL---SKNGSYPSGHTSIGMATLVLAELINPQRONEILKRGYELGESRVICGYH 187
DB 216 PTLVPEKSTNPPSSGCGFPGHTNATTDALALAVAVERYQEWLTRASLGNDRIVAGMH 275
QY 188 WQSDVDARIIVGSAVVATLHTN 209
DB 276 SPLDVGIRVWATRAIASALNN 297

RESULT 10

AB3118
serine protease Atu4566 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AB3118
R:Wood, D.W.; Seubald, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erger, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavhin, T.; Levy, R.; Li, M.; McDaniel
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, B.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AB3118
A:Molecule type: DNA
A:Residues: 1-660 <KUR>
A:Cross-references: UNIPROT:Q8U788; GB:AE008689; PIDN:AAU45360.1; PID:g17743054; GSPDB:C
A:Experimental source: strain C58 (dupont)
C:Genetics:
A:Gene: Atu4566
A:Map position: linear chromosome

Query Match 12.5%; Score 147; DB 2; Length 660;
Best Local Similarity 36.3%; Pred. No. 9.7e-05;
Matches 33; Conservative 17; Mismatches 37; Indels 4; Gaps 1;

QY 139 SKNGSYPSGHTSIGMATLVLAELINPQRONEILKRGYELGESRVICGYHOSDVAARIY 198
DB 288 AKDGGFPGHTNAAVLAIAVAVAVPERFSELTASLGSRIYVAGHSPLDVIGRIT 347
QY 199 GSAVVATLHTNPAPFOOLOKAKDE---FAK 225
DB 348 ATMAAAMLODPKNAEVKAAHDAVEAYFAK 378

RESULT 11

E98169
serine protease Xf0267 [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C:Species: Agrobacterium tumefaciens
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: E98169

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.,
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: E98169
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-660 <KUR>
A:Cross-references: UNIPROT:Q8U788; GB:AE007870; PIDN:AAK8879.1; PID:g15158646; GSPDB:C
C:Genetics:
A:Gene: AGR_L_612
A:Map position: linear chromosome

Query Match 12.5%; Score 147; DB 2; Length 660;
Best Local Similarity 36.3%; Pred. No. 9.7e-05;
Matches 33; Conservative 17; Mismatches 37; Indels 4; Gaps 1;

QY 139 SKNGSYPSGHTSIGMATLVLAELINPQRONEILKRGYELGESRVICGYHOSDVAARIY 198
DB 288 AKDGGFPGHTNAAVLAIAVAVAVPERFSELTASLGSRIYVAGHSPLDVIGRIT 347
QY 199 GSAVVATLHTNPAPFOOLOKAKDE---FAK 225
DB 348 ATMAAAMLODPKNAEVKAAHDAVEAYFAK 378

RESULT 12

F75447
vanadium chloroperoxidase-related protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: F75447
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; i
, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:2003896; PMID:10567266
A:Accession: F75447
A:Molecule type: DNA
A:Residues: 1-145 <WHI>
A:Cross-references: UNIPROT:Q9VU13; GB:AE001953; GB:AE000513; NID:96458740; PIDN:AAF10585
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR1014
A:Map position: 1

Query Match 9.0%; Score 105; DB 2; Length 145;
Best Local Similarity 37.5%; Pred. No. 0.0577;
Matches 24; Conservative 9; Mismatches 31; Indels 0; Gaps 0;

QY 143 SYPSGHTSIGMATLVLAELINPQRONEILKRGYELGESRVICGYHOSDVAARIYSAV 202
DB 77 SYPSGHATVSGAAAEVLAQFFPLQARQLRRDARDAFSSVVGIMHGVGVAGLDVIGRY 136
QY 203 VATL 206
DB 137 ARAL 140

RESULT 13

A87623
PAP2 homolog protein [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: A87623
R:Nierman, W.C.; Feldbljum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolom
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: AB7623
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-259 <STO>
A:Cross-references: UNIPROT:Q9A424; GB:AEO05673; NID:g131424659; PIDN:AAK24981.1; GSPDB:G
C:Genetics:
A:Gene: CCJ019
C:Superfamily: bacitracin transport permease; glucose-6-phosphatase catalytic domain hom

Query Match 8.4%; Score 98.5; DB 2; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.46;
Matches 34; Conservative 13; Mismatches 42; Indels 19; Gaps 3;

Oy 104 AGDIAISAKETWIRPFAFGVSTCNTTEODKLKNKGVSFSGTIGWTALVL----- 159
Db |
 136 SGVTYSGLKAIVGRERDEAVRYVE-----AVNASFFSGHAMLSAVFTLGVI 186
 |
Oy 160 AEINQRONELIKGYE-----LGSRVICGYHMQSDVDARIYGA 201
Db |
 187 ARFSRRRKILVAASAAYVSLVGASRYYLVGVHWSDVLGGWSYGAA 234
 |

RESULT 14

D82070 conserved hypothetical protein VC2488 [imported] - Vibrio cholerae (strain N16961 serogr
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: D82070
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.
charlston, D.; Ermolaeva, M.D.; Yamamoto, U.; Bass, S.; Qin, H.; Dragoti, I.; Sellers,
1, R.R.; Mekalanos, J.U.; Venter, J.C.; Fraser, C.M.
A>Title: DNA Sequence of both chromosomes of the cholera pathogen vibrio cholerae.
A:Reference number: A82035; MUID:2040683; PMID:10952301
A:Accession: D82070
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-178 <HEI>
A:Cross-references: UNIPROT:Q9KP85; GB:AEO04318; GB:AEO03852; NID:g9657063; PIDN:AAF9563
A:Experimental source: serogroup O1, strain N16961, biotype El Tor
C:Genetics:
A:Gene: VC2488
A:Map position: 1
C:Superfamily: bacitracin transport permease; glucose-6-phosphatase catalytic domain hom

Query Match 8.2%; Score 96; DB 2; Length 178;
Best Local Similarity 31.0%; Pred. No. 0.45;
Matches 27; Conservative 13; Mismatches 43; Indels 4; Gaps 1;

Oy 113 KEKYRIIPAFYGVSTCNTTEODKLKNKGVSFSGTIGWTALVLAEINQRONEILK 172
Db |
 81 KNSFGRRRPQLSLALTATITPSDRY----SLPSGTAAATVMATLICITPHMYAVALLC 136
 |
Oy 173 RGYLEGESRVICGYHMQSDVDARIYV 199
Db |
 137 WAGLIGLARVLGVHFLLSDVIAGALLG 163
 |

RESULT 15

T07064 seed biotin-containing protein LEA [validated] - soybean
C:Species: Glycine max (soybean)
C:Date: 01-Sep-2000 #sequence_revision 01-Sep-2000 #text_change 09-Jul-2004
C:Accession: T07064
R:Huang, Y.C.; Tsou, C.H.; Hou, T.F.; Chen, Z.Y.; Heien, K.L.; Heien, J.S.; Chow, T.Y.
Plant Mol. Biol. 38, 481-490, 1998
A>Title: Tissue- and stage-specific expression of a soybean (Glycine max L.) seed-matura
A:Reference number: z15895; MUID:98418627; PMID:9747855
A:Accession: T07064
A>Status: preliminary; translated from GB/EML/DDBJ
A:Molecule type: mRNA
A:Residues: 1-643 <HSI>

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A:Cross-references: UNIPROT:Q39846; EMBL:U59626; NID:G1389896; PID:AAC61783.1; PID:G1389896
C:Experimental source: strain Shi-Shi; cotyledon
C:Superfamily: pea seed biotin-containing protein
C:Keywords: biotin binding; seed
F:125/Binding site: biotin (Lys) (covalent) #status predicted

Query Match      8 0%; Score 93.5; DB 1; Length 643;
Best Local Similarity 27.5%; Pred. No. 4.2; Indels 39; Gaps 9;
Matches 50; Conservative 20; Mismatches 73;

OY 44 QAMVEGRLLRNTERGKLAEDANLSAGGVANAFSSAFG---SPITEKD-APQLHKLLTN 99
Db 165 QVVAEKGR-ETETARGVGAENEGARTTAVITCTLEKGGCTQKPIREERSESESRSAWE 223
OY 100 MIEDAGDIATRSAKERKMRIRPPAFYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVL 159
Db 224 QISNYSQATQGVKEKYEKAKQAA---SETLNTTQTOTAQEKs-----AQAKNL 268
OY 160 AEINPQRONEILKRGVEELGESRVICGYHWQSDVDARIYGSAAVATLHTNPAPFOQQLQKA 219
Db 269 A--AQAKDATLEKGOQ-----GYAVTKDT---ISSAAKTASEKTAPlV---AEKA 309
OY 220 KD 221
Db 310 KD 311

Search completed: March 2, 2005, 20:27:46
Job time : 26.333 secs

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